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Listing first 45 summaries
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Glazov, E.A.

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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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ion "mrcqevkswtekglvaafidlsvafsllcasfivytskelgle
glyseceqeslrnlpvkxissvqbsvknetpedsilynggkercerr
typsygkenkasgedlltaqslkkgsfkvkskrlsehrsygfknhyq
gsydendpllvnsnvnvdedascnivdsgkaledyslrksvslssygcg
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FDEMPERTI IFTWIKMIKELASRRIJIGEVFGLEVRMVSERVTPNERGTFSGVLEACRGGS
VAFDVVEQIHARIIYQGIRDSTVYCNPLIDLYSRNGFVDLARRVFDGLRIKDHSSWA-
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LGFSSDTYVCNALVSLYFHLGNILISAEHIFSNMSQRDAVTYNTLINGLSQCGYGEKAM
                                                            /note="strong similarity to isoflavone reductase-like protein, Lupinus albus, gb:U48590 contains EST gb:T21063, T88563, H36393, AA720215, T76
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TYVLLSNLYAVSKKWDARDLTRQKMKEKGVKKEPGQSWIEVKNSIHSFYVGDQNHPLA
DEIHEYFQDLTKRASEIGYVQDCFSLLNELQHEQKDPIIFIHSEKLAISFGLLSLPAT
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/gene="F18A5.40"
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complement(10627. .13689)
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LYAKCADIETALDYFLETEVENVVLMNVMLVAYGLLDDLRNSFRIFRQMQIEEIVPNQ
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(10627. .13689,13812. .13823))
/gene="F18A5.40"
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/gene="F18A5.40"
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/gene="F18A5.30"
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/gene="F18A5.30"
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/gene="F18A5.30"
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                                                                                                                                                         /gene="F18A5.50"
                                                                                                                                                                                                                                                                                                                        /number=
  /codon_start=1
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                                                                                                                        )oin(17299. .17646,18255. .18495,18615. .18818,19108.
∕gene≖"F18A5.50"
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join(7130. 7298,7473. .8347,8449. .8516,9309. .10812,

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11901. .12098,12231. .12509,12633. .12761,12846. .13061,
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96598 CCAAAGCATTAATTTTTATTTTTTTTTCAGTAAAAGAAATGTCATCGTCAAATTGGAT
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-ma lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambri Laboratory, John Innes Centre, Colney Lane, NR4 70J Norwich, UE-mail: michael.bevan@bbsrc.ac.uk
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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CDS	gene	gene ·	exon						CDS	gene	misc_feature	exon	intron	exon	intron	exon	intron	GACH		intron	exon	intron	GAOII	intron	exon	
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    Direct Submission
Submitted (28-DEC-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
3 (bases 1 to 130299)
                                                                                                                                                            Genomic Sequence For Arabidopsis thaliana Clone T3J11 From Chromosome V, complete sequence
                                                                                                                                                                                             Huang, E.N., Nascimentó, L.U., de la Bastide, M., Preston, R.R., Vil, D.M., Spiegel, L.A., See, L.H., Rodriguez, M.A., Shah, R.S., Shekher, M., Kirchoff, K.A., Baker, J.P., O'Shaughnessy, A., Dedhia, N.N. and McCombie, W.R.
                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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McCombie, W.R.
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3 (bases 1 to 82484)
Town,C.D. and Kaul,S.
Direct Submission
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On Apr 28, 2000 this sequence version replaced gi:7158061.
The assembly overlaps from base 1 to base 41329 with F11P10
                                                                                                                                                      Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598354.
                                                                                                                                                                                                                                                                           Submitted (09-MAR-2000) The Institute for Medical Center Dr., Rockville, MD 20850, U
                                                                                                                                                                                                                                                                                                                                                                                              Rounsley, S.D., Lin, X., Ketchum, K.A., Cros Spriggs, T.A., Mason, T.M., Kerlavage, A.R., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana chromosome
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On Apr 18, 2002 this sequence
Location/Qualifiers
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base 1 on F11P10.
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/map="TEn5"
/clone="T14G11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="T3J11"
/clone_lib="TAMU"
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                                                                              /organism="Arabidopsis/cultivar="Columbia"
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                                  /chromosome="2"
                                                           /db_xref="taxon:3702"
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clone T14G11 map
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Adams,M.D.,
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/note="T14G11.11" complement(join(<1125711481,1160711720,1181512042, 1213112247,12320>12385))	/gence"At2333980" //codon_start=1 /product="expressed protein" /protein_id="axa67616_2" /db_xref="GI:20196908" /translation="MXSGASAASPTAKSFNFGSSRLLALAQQLRVYKPPLSSSFDERE /translation="MXSGASAASPTAKSFNFGSSRLLALAQQLRVYKPPLSSSFDERE /translation="MXSGASAASPTAKSFNFGSSRLLALAQQLRVYKPPLSSSFDERE /translation="MXSGASAASPTAKSFNFGSSRLLALAQQLRVYKPPLSSSFDERE /translation="MXSGASAASPTAKSFNFKAAVLICLFEGDDGDLRVILTKRSSTLS THSGEVSLPGGKAEEHDKDDGTTATREAEEEIGLDPSLVDVYAFLEPFLSQHLLRVIP VYGILWDRKAENDTPWBAEUEAVLDAFFEMFLKDENKRSEEFDWMGEKHLVHFFDYKT GDSDYVIWGLTARILIRAATVVYQRPPAFIEQKPNLKYSKMNQATRLYGWLKPLANLH ESCENGRILGHVPAYCLRYLYGISSR" complement(1125712385) /gene="At2333990"	595)) 025,91299 95))	/yelle" AL293300 / Al293300 / Al293300 / Al293300 / Al293300 / Al293214G11.10; predicted by genefinder; supported by CDNA: gi_15293224_gb_AY051046 1_" complement(join(<75107581,89359025,91299326,	72767347 72767347 /gene-"At2g33970" /product="tRNA-Pro" complement(751010595)	/gene="At2g33960" /product="tRNA-Pro" 7276. 7347	68106881 /gene="At2g33960" 68106881	/gene="At2g33950" /gene="At2g33950" /product="tRNA-Pro"	/product **ENA-Pro** /product **ENA-Pro** 58925963	/gene="At2g33940" 48534924 /neno="ht2g33940"	/gene"Atzg33930" /product="txNA-pro" 48534924	44114482 /gene="R42933930" 4411	/gene="At2g33920" /product="tRNA-Pro"	38983969 /gene="At2g33920"	29463017 /gene="At2g33910" /product="RNA-Pro"	/product case fro 2946. 3017 /gene="At2g33910"	/gene="At2g33900" 2114. 2185 /gene="At2g33900" /product="*BDA.DOO"	18	/gene="At2g33890" 1141. 1212	11844 /note="overlap with BAC clone T1B8 (U78721:102301114144)." 11411212	_
repeat_region gene		CDS	mRNA	gene		CDS	mRNA	gene			CDS	mRNA		repeat_region	repeat_region				CDS	
2454424589 /rpt_family="(GAGAA)n" complement(2614628119)	/Codon_stait=1 /product="unknown protein" /product="unknown protein" /protein_id="AAB67620.1" /protein_id="AAB67620.1" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:2342722" /db_xref="g1:23427250 /fd-xref="g1:23427250 /fd-xref="g1:	/gene="At2g34020" complement(Join(2234222978,2307823217,2372423905, 2402924458) /gene="At2g34020"	/gene="Artg34020" /note="T14G11.14; similar to T14G11 15" complement(join(<2234222978,2307823217,2372423905, 24029>24458))	/ LIGHT ACTURE TO COMMIT SOUS TO ENAUGHDES SOUR VERNOR PER VER PER VER PER VER PER VER PER VER PER VER VER VER VER VER VER VER VER VER V	/product-"hypothetical protein" /protein_id-"AAB67619.1" /db_xref-"61:2342721"	join(19624. 19940,2049320631,2070920888) /gene="At2g34010" /codon start="	/gene="At2g34010" /note="T14G11.13; predicted by genscan" join(<1962419940,2049320631,20709>20888) /gene="At2g34010"	FETENDRINGERREPROGESHASS Y LAME FOR STAFFMENDE SENDELEGE POLGGIFFRING VIKVLPNUMHRIPDEGIGKWLESHATCPVCRRLAEPHTSNGDKVLERIV* 1962420888	/db_xref="G1:2342720" /translation="MGFNDPSLNTIILWFASVTSLVTISVIFALLIICLLKRRRFDVS	/gene="Ar2934000" /codon_start=1 /product="hypothetical protein" /protein_id="AAB67618.1"	/gene="At2g34000" 15932".16387	/gene="At2g34000" /note="T14G11.12; predicted by grail" <15932>16387	/rpt_family="AT_rich" 15932	1452914597 /rpt_family="(A)n" 14676. 14736	KIVSLSSVPAKITYEVGAKKIVKFKKLSEVGA". complement(1309213112) /rpt_family="AT_rich"	SEDWAATRIQTAFKAYKAAKSLRKLKGIARAKLSTEKQSVKNQAVTTLRYLHSWSKIQ SEIKARRVCMVTEWRLKNKRLEHOOKLEAKLHDVSVEWNGGSETKDEILERILQREEA TIKRERALAYAFSHQLGNTNWGWSWKERWISARPWEVRYSVTPKKPKSSKTDSNSPAK	/protein_ig="AAB0/01/.1" /db_xref="G1.2342719" /translation="MGSGNLIKAIIRLKKSKQGTEKKKTSAVKPKKGSKKKGTSLVTR	<pre>/codon_start=1 /product="putative_SF16 protein (Helianthus annuus)"</pre>	/gene="At2g33990" complement(join(1125711481,1160711720,1181512042, 1213112247,1232012385)) /gene="At2g33990"	

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AX375189
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Eukaryota; M
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
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/gene="At2g34030"
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/protein_id="AAB67621.1"
/protein_id="AAB67621.1"
/db_xref="Gi:2342723"
/translation="MAGVTLFFSLLSIALIISGVSSRVLISHVPLNNSILISDGIHDA
/translation="MAGVTLFFSLLSIALIISGVSSRVLISHVPLNNSILISDGIHDA
/LHEFLTLDFFSLSKRACVHVGGILFBLAMLUSTGLSLSRDVASSFIDDNVGLTVFSLSEGS
KLFVLFBVFVGGIIFPLTMKFPRIALMLSTGLSLSRDVASSFIDDNVGLTVGHTVFS
KLFVLFBVGFVGGIIFPLTMKFPRIALMLGTGLSLSRDVASSFIDDNVGLTVGHTVST
KLFUFFVGGIIFPLTMKFPRIALMLGTGLSLSRDVASSFIDDNVGLTKEFS
KHIIKDGELSKESLKSLFKKTONKDGKIQISELDLFTEGMFVLKLKFFSF
KHIIKDGELSKESLKSLFKKTONKDGKIQISELDLFTEGMFVLKKFTSF
LEDFDGDUNGELERNFFEGGIARLLKQYKFNVEDQRENGTEENGVLKLEKFKTVTN
KLLSMETLIATTEVIVGILIVLFLAKFFMLNIQLLSISAGIPSFYIVFAMIPFARNLK
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                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
759 c 950 g 119
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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                         10.6%;
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73.6%;
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  Score 111; DB (
Pred. No. 8e-18;
0; Mismatches 2
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Pred. No. 7.3e-26;
0; Mismatches 70;
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     225;
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                                               Length 4299;
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                                                                                                                                                                                                                                                                                                                      gene silencing
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Sequence 4158 1
AX333649
AX3333649.1 GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene sets
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AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTTGCGACTGTCCAGATATGTGTAGATAGT
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                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
889 c 1129 g 150
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from Patent W00194629.
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Pred. No. 8e-18;
0; Mismatches 225;
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Best Local Similarity 54...
Matches 272; Conservative
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                                                                                                                                                                              MATSUMOTO, T., GOTO, M. and FUTUICH1, Y.

DETECTION OF MUTATION IN PATHOGENIC GENE OF HUMAN WERNER SY
LEIJIIN KENKYUSHO:KK

OS Homo sapiens (human)
JP 1998201498-A/1
PD 04-AUG-1998
PF 24-JAN-1997 JP 1997011268
PF 4ATSUMOTO TAKEHISA, GOTO MAKOTO, FURUICHI YASUHIRO PC C1201/68,C07H21/04,C12N15/09,G01N33/50,G01N33/566; CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH Key JOTOGUCTE'WS'
FT CDS /producte'Ws'
FT CDS /producte'Werner's syndrome'.
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1 (bases 1 to 5189)
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1. .5189
                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
889 c 1129 g 150
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0; Mismatches 2
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Yu.C.-E., Oshima,J., Fu,Y.-H., Wijsman,E.M., Hisama,F., Matthews,S., Nakura,J., Miki,T., Ouais,S., Martin,G.M., and Schellenberg,G.D.
Positional cloning of the Werner's syndrome gene Science 272 (5259), 258-262 (1996)
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Homo sapiens Werner syndrome
L76937
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Homo sapiens DNA.
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LTDVANKKLKCTETWSLNSLVKHLEGKQLLKDKSIRCSNWSKFPLTEDQKLVAATDAY
AGFIIYNLEILDDTVQRFAINKEEEILLSDMMKQLTSISEEWMDLAKHLPHAFSKLE
NPRRVSILLKDISENLYSLRRMIIGSTNIETELRPSNNLNLLLSFEDSTTGGVQQKQIR
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232 4530
/note="unnamed protein product"
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/db_xref="taxon:9606"
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                                                Homo sapiens WRN (WRN) mRNA, AF091214
AF091214.1 GI:3719420
    Homo sapiens
                                                                                                                      AF091214
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RKTGNILODLOPFIVKTSSKHKEE EGPTI IYCDSRKMTQQVTGELRKLNLSCCTYHAGM
SFSTRKDIHHREVRDEIQCVIATIAFGMGINKADIRQKIHYGAPKDMESYYQEIGRAG
RDGLQSSGHVLMAPADINLNRHLLTEIRNEKFRLYKLKMMAKNEKYLHSSRCERQIIL
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HCYNQVPVELSTEKKSNLEKLYSYKPCDKISSGSNISKKSIMVQSPEKAYSSSQPVIS
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AQEQETQIVLYGKKULPBARQKHANKMYVPPAILATNKILVDMAKMRPTTVENVKRIDGY
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5159. .5164
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YSLFQEKKMPIKSIAESRILPIMTIGMHLSQAVKAGCPLDLERAGLTPEVQKIIADVI
RNPPVNSDMSKISLIRMLVPENIDTYLIHMAIEILKHGPDSGLQPSCDVNKRRCFPGS
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ENVLTDIKLGKYRIVYVTPEYCSGNMGLLQQLEADIGITLIAVDEAHCISEWGHDFRD
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MSLDITEHELQILEQQSQEEYLSDIAYKSTEHLSPNDNENDTSYVIESDEDLEMEMLK
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516 AATTATTGTGATGTTATGCATATTTTT----CATTCTGGTATCCCTCAAAGTCTCCAACAT 572
                                                             493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTTTTCTGAG
                                                                                                                                                                                                                                396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTTGGCTTGGATATTGAGTTGGAGACCA 455
                                                                                                                                                                                                                                                                                                                           272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Street SE, Bothell, WA 98021, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Alisch, R.S., Mulligan, J.,
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                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                          AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT
                                                                                                                                                                                              GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1681
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                                                                                                                                                                                                                                                                                                                               Conservative
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RKTGNILQDLQPFLVKTSSHWEFEGPTIIYCPSRKMTQQVTGEKLNLSCGTYBAGM
SFSTRKDIHREVRDBIQCVIATIAFGMGINKADIRQVIHYGAPKDMESYYQEIGRAG
RDGLQSSCHVLMAPADINLNRHLLTEINNEKFRLYKLKMMAKMEKYLHSSRCRRQIIL
SHFEDKQVQKASLGIMGTEKCCDNCRSRLDHCYSMDDSEDTSMDFGPQAFKLLSAVDI
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CVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQMKLLRDFDIKLKNEVE
LTDVANKKLKCTETWSLNKHLLSENGLGKQLLKOKSIRCSNMSKFPLTEDQKLYAATDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLSPNDNENDTSYVIESDEDLEMEMIKSLENLNSGTVEPTHSKCLKMERNLGLPTKEE
EEDDENEANEGEEDDDKDFLMPAPNEEQVTCLKMYFGHSSFKPVQMKVIHSVLEERRD
NVAVMATGYGKSLCFQYPPVYVGKIGLVISPLISLMEDQVLQLKMSNIPACFLGSAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEICSSSKRSKEEVGINTETSSAERKRRLPVWFAKGSDTSKKLMDKTKRGGLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEGKAAMLAPLLEVIKHFCQTNSVQTDLFSSTKPQEEQKTSLVAKNKICTLSQSMAIT
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AQEQETQIVLYGKLVEARQKHANKMDVPPAILATNKILVDMAKMRPTTVENVKRIDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGEKFGIGLPILFLRGSNSQRLADQYRRHSLFGTGKDQTESWWKAFSRQLITEGFLVE
VSRYNKFMKICALTKKGRNWLHKANTESQSLILQANEELCPKKFLLPSSKTVSSGTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENVLTDIKLGKYRIVYVTPEYCSGNMGLLQQLEADIGITLIAVDEAHCISEWGHDFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSLDITEHELQILEQQSQEEYLSDIAYKSTEHLSPNDNENDTSYVIESDEDLEMEMLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="WRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Werner syndrome"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC63361.1"
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                                                                                                                                                                                                                                                                                                                                                          Score 111; DB 9
Pred. No. 8e-18;
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J., Galas,D.
                                                                                                                                                                                                                                                                                                                               Mismatches
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D. and Fu,Y.-H.
                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 5208;
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REFERENCE
AUTHORS
TITLE
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AF067418
LOCUS
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AUTHORS
TITLE
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SOURCE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                     Submitted (20-MAY-1998) Fox Chase Cancer Avenue, Philadelphia, PA 19111, USA
                                                                                                                                                                                                                                                                                                                                                                   Yan, H., Chen, C.Y.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC
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LH., Chen,C.Y., Kobayas
Lication focus-forming
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/product="focus forming activity 1"
/protein_id="AAC63512.1"
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/db_xref="G1:3420291"
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CXLFHLSPMAGFPKGLKRLLEDESVERKYSVGCSWADIFLITEDGLYAATDAYAGLLIQ
KKLECKEKWTFNGLIKHLFKEDLYKRKSYFGCSWADIFLITEDGLYAATDAYAGLLIQ
KKLECKELMENESVFRVGFGSVADLYKRKSYGLTDLSKCLMDLVNQVPNSFGCYTEAVRA
VDILEDLSEKLEELRNIMKEASKAEGNGLHFQNSEDCSKKDKSILHVACKESLAEHKM
DCKNAADSQNNKDIDSCQNENRDEDFFMTLGISEEELYMMEREDDKKQTNPDYKLNKDS
                                                                                                                                                                                                              /gene="FFA-1"
160. .4470
                                                                                                                                                             /codon_start=1
                                                                                                                                                                            /gene="FFA-1"
/function="DNA helicase"
                                                                                                                                                                                                                                                           /cell
                                                                                                                                                                                                                                                                          /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                         _type="oocyte"
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                               ACCESSION
VERSION
KEYWORDS
                                                                                            RESULT 14
ATFCA0/c
LOCUS
DEFINITION
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KTTNISIDLROPLIKKOQGSGWEFEGATIVYCEPTKTSEQVTAELIKLGIAGTYHAG
MGIKQRREVHHRFMRDEIHCYVATVAFGMGIUNEDIRKYHYGAPKEMESYYQEIGRA
GRDGLPSCCHALMAQADMNENRHMLGEIPNKGFREYKLKMLTKMEKYLMSSTCRKII
LSHFEDKQLEKASSGIMGTEKCCDNCKTRLICNISINDTEDNLQDFGPQAYKFISAVD
VLGQKFGTGVPVLFLRGSTSQRVPDRFRNHSLFSSGKDQTEAFWKVLARQLITEGYLQ
ESSGGTKFSTICGLTSKGSNWLIKANNEQCPSLLLPSNBELCLQRTRVSNFSSAQAHS
SMVPHASSNTRSSMPKAGPEKMELKDKRSYQGAERLSKAAGVSKSSFKLQTPCKLSRP
PEPEYSPRERELQTTLYGRLVVARQKIASERDILAVLATNKVLYDMAKLRFTSEM
KKLDGVSEAKSAMLAPLLEVVKEFCIANSLKUDYFSGSVSQSESTFTPREQERISLP
ESQRNSYSLFGQNLSLKKIADVRCLSMAVVGMHLMQALKAGYSSGAQGQPEFPTQ
ETTYAIKKPPINSDLSSFKAIREYVFANIDGYPIRMVISLLEKEGSGAQGOPEFPTQ
KTLIQTEENPKNVSVQNTKHKVTMGKSMWIEKKPTQPATAELEVTKGKALAPIMLASW
NEASLDADTEELFSESQSSTTRPRRRLPEWFGSTKGNAATRCIQESKNLGEEKGSFFD
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EEEDEGIEEEDDDDDDWDPSMPEPSAQHLSCLKTYFGHSSFKPVOMKVVHSVLRERRDN
LVVMATGYGKSLCYQFAPVYTSGIGIVICFLISLMEDQVLQLEMSNISSCFLGGAQSK
NVLQDVKDGKMRVIYMTPEFCSRGISLLQDLDMRYGITLIAIDEAHCISSMGHDFRSA
YRSLGSLKRMLPNVPIVALTATASPSIREDITKSLNLHNPQVTCTSFDRPNLYLDVAR
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GATTCCTTCCGTGTTGGCAGA
                                                           GATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGCTGTCAGT
                                                                                                                                                                                          GTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATC
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                     GGCTCATAACGTGAAGGAGGA 920
                                                                                                            AGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGCAGTTACAATACGCAGCAACG
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                                              GATGCTTATGCTGGGCTACTCATTTACAAGAAACTAGAGGGCATGGATGCTCACGAGAGT
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SOURCE ORGANISM

Arabidopsis Arabidopsis

thaliana thaliana

Arabidopsis thaliana DNA chromosome No. 0. E297335 Z97335.2 GI:5280985

ATFCA0

200576 bp

DNA,

linear ESSA I FCA

contig fragment

PLN 28-JUN-1999

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JOURNAL REFERENCE
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Dn Jun 30, 1999 this sequence version replaced gi:2244747.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thai/this fragment has an overlap with ATFCAl at the 3' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPDSDLMLILQTTAKWRNNTDCCSWGGISCDFKTGVVVELDLGNSDLNGRLRSNSSLF
RLQHLQSLDLSYNDLSCTLPDSSGNFKYLRVLNLLGCNLFGEIFTSLRSLSYLTDLDL
SYNDDLTGEILDSMGNLKHLRVLSLTSCKFTGKIPSSLGNLTYLTDLDLSWNYTTGEL
                                                                                                                                                                                                                                                                                                                                                         TDFQLMLLNLSSLTNVDLSSNQFKAMLPSNMSSLSKLEAFDISGNSFSGTIPSSLFML
PSLIKLDLGTNDFSGPLKIGNISSPSNLQELYIGENNINGPIPRSILKLVGLSALSLS
FWDTGGIVDFSIFLQLKSLRSLDLSGINLNISSSHHLPSHMMHLILSSCNISQFPKFL
/gene="dl3000w"
                                                                                                                                          MRIFSCFSSPLKK"
                                                                                                                                                                                                                     MELVGSGFEIYKTIDVSGNRLEGDIPESIGILKELIVLNMSNNAFTGHIPPSLSNLSN
                                                                                                                                                                                                                                            INCSYLQFLNVEENRINDTFPSWLKSLPNLQLLVLRSNEFHGPIFSPGDSLSFSKLRF
FDISENRFSGVLPSDYFVGWSYMSSFVDIIDNTPGFTVVGDDQESFHKSVVLTIKGLN
                                                                                                                                                                                                                                                                                                  ENQTSLYHLDISANQIEGQVPEWLWRLPTLSFIASDNKFSGEIPRAVCEIGTLVLSNN
NFSGSIPPCFEISNKTLSILHLRNNSLSGVIPEESLHGYLRSLDVGSNRLSGQFPKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="disease resistance Cf-2 like protein"
/protein id="CAB10171.1"
/protein id="CAB10171.1"
/db_xref="GI:2244748"
/db_xref="GI:2244748"
/tbranslation="MITTIWSLCLIFCLSNSILVIAKDLCLPDQRDALLEFKNEFSIP
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/gene="d13000w"
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/clone="BAC TAMU6G17"
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/variety="Columbia"
                                                      'number-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similarity to Cf-2.2, Solanum pimpinellifolium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="dl3000w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
db_xref="taxon:3702"
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                                                                                                                                                                 .CGAPLQKKCGGEEEEDKEKEEKDKGLSWVAAAIGYVPGLFCGLAIGHILTSYKRDWF
                                                                                                                                                                                        QSLDLSQNRLSGSIPGELGELTFLARMNFSYNMLEGPIPQGTQIQSQNSSSFAENPG
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SAAVFAWKGETLQEYWWCTERALDWGPGGGPDLIVDDGGDATLLIHEGVKAEEIFEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEPV$$WGNT$LV$VDPBIHDLIEKEKRRQCRGIELIASENFT$
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VNFTTGYIDYDKLEEKALDFRPKLLICGG$AYPRDWDYARFRAIADKVGALLLCDMAH
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hydroxymethyltransferase (EC 2.1.2.:
contains EST gb:1565775"
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                                                                                                          GRLMNLGCATGHPSFVMSCSFTNQVIAQLELWNEKASGKYEKKVYVLPKHLDEKVALL
                                                                                                                                                           CAAAMKTAGARVIYTEIDPICALQALMEGLQVLTLEDVVSEADIFVTTTGNKDIIMVD
                                                                                                                                                                                     GQVPDPTSTDNPEFQIVLSIIKEGLQVDPKKYHKMKERLVGVSEETTTGVKRLYQMQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(12823. .13533,13822. .14568)
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/gene="d13005c"
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QIVTNGTENHLVLMDLRPLGLTGNKVEKLCDLCSITLNKNAVFGDSSALAPGGVRIGA
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                       12823. .13533
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                                                                                                                                    HMRKMKNNAIVCNIGHFDNEIDMLGLETYPGVKRITIKPQTDRWVFPETKAGIIVLAE
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/gene="dl3000w"
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'gene="d13020c"

complement(join(18573. .18914,18997. .19137,19212.

19603. .19719,19762. .20123))

'gene="d13020c"

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19603. .19719,19762. .20123))

'gene="d13020c"

'note="weak similarity to fusion protein la/lb - su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:023256"
/translation="MENSTALVIFALIFILISADAFPIPSPNGEIDAMLIRNSIIGED
EDLAMCTEISREVLMAQKELTTIVALDKLILTAEAVTPLPDALETQTTSTHEGKI
QEIAKIGSFLAEASKLYD"
complement(16093...16270)
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/gene-"d13015c"
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/gene="dl3015c"
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/gene="d13015c"
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/db_xref="GI:2244752"
/db_xref="SPTREMBL:023257"
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Best Local Similarity 53.2%;
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1 (bases 1 to 6476)

1 (bases 1 to 6476)

Guarente,L.P. and Sinclair,D.A.

Assays for compounds which extend life span

Patent: US 6228583-A 5 08-MAY-2001;
                                                                                                                                                                                                             GGGGCCTTGCCTCACCTGAGGACACTTGTTTGCAAAGAGCCTCCTGAAGCCCAAACAGAA 777
                                                                                                                                                                                                                                                                           TCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAAT 717
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                                                                CTGATGCTTATGCT
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                                                                                                                                                            TCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAA 837
                                                                                                                                                                                            GGAGCCTCAATGGTCTGGTTAAACACGTCTTAGGGAAACAACTTTTGAAAGACAAGTCCA
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Pred. No. 1.5e-10;
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Listing first 45 summaries
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8103	5433	681	17534	3595	439	439	439	439	439	439	439	439	439	1500	1500	1499	580073	15674	15674	15674	13059	2155561	690	651	3149	3149	3149	2833	814	449	29604	5058	4792	4206	1164
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ABL33661	AAA99265	AAH03262	ABK40025	ABK84215	ABS15980	AA108383	AAI48016	AAI22718	AAK41953	AAK16207	ABA34854	ABA67796	ABA49878	AAD05663	AAZ37307	AAZ37308	AAT58840	ABL34476	ABL32362	ABL70513	AAV74531	ABN71527	ABN69471	ABN70543	ABA90939	AAS59270	AAX90441	AAH14483	AAH06496	ABA08508	AAX83005	AAV35114	AAX83004	AAV35115	AAV35131
Human immune syste	Plasmodium yoelii	Human cDNA clone (Human chemically p	Human cDNA differe	Human genome-deriv	Probe #8374 used t	#16702 used	Probe #12651 for g	Human bone marrow	brain e	#13320		4	thali		Arabidopsis Abi4 c	a	Human metastasis a	Human immune syste	Chemically treated	aur	Streptococcus poly	Streptococcus poly	Streptococcus poly		Human cDNA encodin		Human cDNA sequenc	_	Human secreted pro	al mo	Mouse WRN helicase	Mouse WRN coding s	e WRN helicas	Mouse WRN helicase

ALIGNMENTS

RNase D; enzyme; 3'-5' exonuclease; gene expression; plant; gene silencing; transgenic plant; gene; ss. Levin JZ, (SYGN) SYNGENTA PARTICIPATIONS AG. (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL. 01-AUG-2000; 2000US-222202P 30-JUL-2001; 2001WO-EP08825 Arabidopsis thaliana. Arabidopsis RNase D related domain (3'-5' exonuclease domain) cDNA. ABA91805 standard; cDNA; 1049 Phillips KL, (first entry) Location/Qualifiers 42..908 /*tag= a /product= "3'-5'_exonuclease_domain" /*tag= Budziszewski GJ, Meins F, ВP Glazov EA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present nucleotide sequence comprises cDNA encoding an CC Arabidopsis thaliana 3'-5' exonuclease domain (see AAM50937), CC specifically an RNase D related domain. The cDNA was identified CC on the basis of homology to the 3'-5' exonuclease sequence given in CC ABA91795 via 3'-and 5' RACE and TA-cloning. The sequence is nearly CC identical to an Arabidopsis exonuclease termed wrnexo. Nucleotide CC (see ABA91795-807) and polypeptide (see AAM50927-39) sequences for CC 3'-5' exonuclease domains were identified using different screening methods and search algorithms. The invention encompasses the cuppression or increase of gene silencing in plants. This is CC achieved by altering the expression in the plant cell of a nucleotide sequence encoding a polypeptide comprising an exonuclease domain, preferably a 3'-5' exonuclease domain, and especially an CC altered by altering its transcription or translation. It is CC altered by altering its transcription or translation. It is CC altered by altering its transcription or translation. It is CC aptamers, zinc finger proteins, double-stranded RNA, or insertional, CC aptamers, zinc finger proteins, double-stranded RNA, or insertional, CC aptamers, zinc finger proteins, double-stranded RNA, or insertional, CC aptamers, contained a sequence of interest in a plant cell or plant. Suppression or decreasing expression of the nucleic acid molecule cc results in decreased levels of post transcriptional gene silencing and improved expression of genes of interest.
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P-PSDB; AAM50937.
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                       TAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGG
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The present nucleotide sequence encodes an Arabidopsis thaliana 3'-5' exonuclease domain (see AAM50927), specifically an RNase D related domain (GenPept accession CAB36851). The nucleotide sequence is found in BAC F18A5, GenBank accession number ALJ03528.2. Nucleotide (see ABA91795-807) and polypeptide (see AAM50927-39) sequences for 3'-5' exonuclease domains were identified using different screening methods and search algorithms. The invention encompasses the suppression or increase of gene silencing in plants. This is achieved by altering the expression in the plant cell of a nucleotide sequence encoding a polypeptide comprising an exonuclease domain, preferably a 3'-5' exonuclease domain, and especially an RNase D-related domain. Expression of the nucleotide sequence is

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                                                                      CTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAG
                                                                                             GGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTC
                                                                                                                                            GATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCAT
                                                                                                                                                                                                                                             TGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAA
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                    TTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGAC
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Pred. No. 2.4e-233;
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RESULT
ABA9180
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       The present nucleotide sequence is that of human DNA encoding Werner syndrome protein (see AAM50935), the N-terminal portion of which comprises a 3'-5' exonuclease domain. The sequence was comprised the basis of homology to an Arabidopsis 3'-5' exonuclease domain (see AAM50927). The invention provides nucleotide (see AAB91795-807) and polypeptide (see AAM50927-39) sequences for CC see ABA91795-807) and polypeptide (see AAM50927-39) sequences for CC suppression or increase of gene silencing in plants. This is CC achieved by altering the expression in the plant cell of a compasses the CC domain, preferably a 3'-5' exonuclease domain, and especially an CC RNase D-related domain. Expression of the nucleotide sequence is CC modulated by altering its transcription or translation. It is CC modulated by altering its transcription or translation. It is CC modulated by altering its transcription or translation. The use of ribozymes, domainant-negative mutants, CC aptamers, zinc finger proteins, double-stranded RNA, or insertional, CC opint or deletion mutagenesis, and increased by overexpression of CC suppressing or decreased expression of the nucleic acid molecule cc suppressing or decreased levels of post transcriptional gene silencing CC and improved expression of genes of interest.
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                                                                                                                                                                                                                                                                                                                                                                         Claim 42; Page 85-86; 102pp; English.
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                  Detection of mutation in gene causing human Werner's syndrome oligo:nucleotide used for detection, comprises amplifying DNA synthesising oligo:nucleotide
                                                                                                     WPI;
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Pred. No. 9.1e-22;
0; Mismatches 225;
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RESULT 7
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DT 15-N
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EN Lung
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EN EUNG
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EN EUNG
EN EUN
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stomach; lun cytostatic; gene; ds.

Homo

sapiens

Lung

cancer related gene sequence

SEQ

IJ

NO:4158

15-MAY-2002 ABL65821; ABL65821

(first

entry)

standard;

DNA;

5189

ΒP

910

TTAGAGATTTTGGATGATACTGT

Human; cancer; colon; breast; ovary; oeso; stomach; lung; prostate; pancreas; carcing cytostatic; gene therapy; antineoplastic;

carcinoma; antitumour; cancerous; oesophagus; kidney; thyroid

Wilm's

tumour;

adenocarcinoma;

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Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a gene, the mutation of which causes werner's syndrome. The specification describes the detection of a mutation in a gene causing human Werner's syndrome. The method comprises amplifying a DNA fragment containing a mutation at position 733, 734, 1620 or 4146 of AAV65701 or at position 42 of AAV65702 and synthesising an oligonucleotide so that the base at the above site comes to be the 3 end based on the base sequence of AAV65701-02, or an oligonucleotide in which the base adjacent to the 3 end comes to be the 5 end. The oligonucleotides are hybridised with the resultant amplified fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
                                                    AAGCAGCAGTTACAATACGCAGCAACGGATGCTTTATGCTTCATGGCATCTTTACAAGGTT
                                                                                                                                                                                                                                TIGCITGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA
                                                                                                                                                                                                                                                                                                                  CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                   AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCCAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATATTAGCATGAGTCTATCAGATGGGGGATGTGGGGATTTGACATGGAGTGGCCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5189 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pages 10-11;
   CTTAAGGACCTTCCTGATGCTGT
                                   AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCACT
                                                                                                                                                                   AAAAAGCTGAAATGTACAGAGACCTGGAGCCTTAACAGTCTGGTTAAACACCTCTTAGGT
                                                                                                                                                                                                CAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC
                                                                                                                                                                                                                                                                 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT
                                                                                                                                 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGGAACTGGGAGTTTTATCCTCTGTCA
                                                                                                                                                                                                                                                                                                                                                                  AGCAAATGTTACTTGTTCCACGTTTCCTTCCATGTCAGTTTTTCCCCCAGGGATTAAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                               TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTTTTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1663 A; 889 C; 1129 G; 1508 T; 0 other;
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54.1%;
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     895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
).9e-22;
les 225;
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18-SEP-2000
20-SEP-2000
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29-SEP-2000
29-SEP-2000
29-SEP-2000
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29-SEP-2000
21-CCT-2000
The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical
                                                                                                                                                                                                                                                                                                                                                      Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature generation of the control of th
                                                                                                                                                                                                                                                                                                                 Claim
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2000US-244867P.
2000US-245084P.
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2000US-237598P.
2000US-237604P.
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2000US-237295P.
2000US-237316P.
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2000US-235638P.
2000US-235711P.
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2000US-236032P.
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2000US-235082P.
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2000US-234567P.
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Best Local :
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                                                                                                                                                                                                                                Homo
12-APR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                           Human
                                                                         30-DEC-1996;
                                                                                                                                                                                WO9724435-A1
                                                                                                                                                                                                                                                                               Human; WRN; Werner's recessive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX83001 standard;
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                                                                                                                                                                                                                                                                                                                                                      WRN coding
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                                                                                                                                                                                                                                                                            Werner's syndrome; isorder; phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
96US-0632175
95US-0009409
                                                                            96WO-US20785
                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5208
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BP.

detection; diagnosis; autosomal;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA
TTAGAGATTTTGGATGATACTGT
                                                                                  GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTATTATTTACCGAAAT
                                                                                                                          AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT
                                                                                                                                                                      AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT
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                                                                                                                                                                                                                                                                                                 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC
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                                                                                                                                                                                                                                                                                                                                                                   CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                           TTGCTTGAAAATAAAGCAGTTAAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA
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                                        CTTAAGGACCTTCCTGATGCTGT
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No. 9.9e-22;
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Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29+DEC-1995;
30+JAN-1996;
30+JAN-1996;
 07-JUN-1999
                                                                     AAX24302 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the coding region for the human WRN gene encodes a protein related to Werner's syndrome. The products can for the detection and treatment of Werner's syndrome (WS), an autorecessive disorder with a complex phenotype, as well as related dispersions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                  AAX24302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding the WRN gene product useful for detection and treatment of Werner's syndrome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fu
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DB; AAY14517.
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OSHIMA
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                                                                                                                                                                                                                                               AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT
                                                                                                                                                                                                                                                                                                                   AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA
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96US-0010835.
96US-0594242.
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entry)
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Pred. No. 9.9e-22;
                                                                     ВP
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                                                                                   494
                CTTCCATGTCAGTTTTCCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGA
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This is the nucleotide sequence of the mWRN gene, the murine thomologue of the human WRN gene associated with Werner's syndrome. CC A claimed assay for identifying a compound which extends life span ccomprises administering a compound to be tested to a mammal with a comprises administering a compound to be tested to a mammal with a comprises administering a compound to be tested to a mammal with a compound to the normal phenotypes of ageing in the mammal. The compound compound compound the normal phenotypes of ageing in the mammal. The compound c
                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying agents that inhibit replication and accumulation of circles - as potential agents for increasing the life span of
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span;
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DB; AAW97841.
                                                                                                                                                                                                                                                   Similarity
                                                                                                         GGAAGGTTGCGACTGTCCAGATATGTGTGATGTAAGTAATTATTGTGATGTTATGCATATTT 540
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TT----CATTCTGGTATCCCTCAAAGTCTCCCAACATCTTATTGAAGATTCAACACTTGTAA
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                                                                        GCAGAGTCGCAGTGATCCAGTTGTGTGTGTCTGAGAACAAATGTTACTTGTTTCACATTT
                                                                                                                                                                                                                                                                                                                                                         6476 BP; 2019 A; 1300 C; 1389 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0054629
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/*tag= d
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229..4434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS
                                                                                                                                                                                                                                                7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sinclair DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                           Score 82.8; DB 20; Pred. No. 2.1e-13; 0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                         1768
                                                                                                                                                                                                                                                                                                                                                         Ŧ,
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mWRN nucleic
                                                                                                                                                                                                                                                                                        6476;
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                                                                                                                                                                                                                   Gaps
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777

889

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RESULT 10
AAV35131
ID AAV35
XX AAV35
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XX MOUSI
XX MEN
DE MOUSI
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XX WEIN
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XX JP1 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                        Query Match 7.7%;
Best Local Similarity 52.9%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                            This sequence is a fragment of novel mouse WRN helicase protein which is associated with Werner's syndrome and has been generated by RACE (rapid amplification of cDNA ends). The mouse WRN gene is useful for the diagnosis of human Werner's syndrome.
                                                                                                                                                                                                                                                                                                       Sequence 1164 BP; 343 A; 223 C; 288 G; 310 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP10146188-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV35131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV35131 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 26-27; 30pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    werner's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mouse gene encoding protein - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EIJI-) EIJIN KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Werner's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse WRN helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998-369863/32
                          598
                                                                                                                                            449
                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    674
AGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCCATGACTATGGAGTTAGTA
                                                                                                                                                                             GGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGATGCTTATGCT 851
| |||||||||||
| CTGATGCTTATGCT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTAACAATACGCAGCAA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAA
                                                             CTTCCATGTCAGTTTTCCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGA
                                                                                                 TT---CATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAA
                                                                                                                                          GCAGAGTCGCAGTGATCCAGTTGTGTGTGTCTGAGAACAAATGTTACTTGTTTCACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGCTGCAGCAATTGGAGTAATTTCCCCCCTCACTGAGGACCAGAAACTGTATGCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGCCTCAATGGTCTGGTTAAACACGTCTTAGGGAAACAACTTTTGAAAGACAAGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAGAGTTTTGTGGAGCTGACGGATGTTGCCCAATGAAAGTTGAAGTGCGCAGAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAAGATGTTGAGGATCTTTCAGATTTAGCCAAACCAAAAAATTGGTGGAGATAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCAGGGGTTGGGATTGAAGGGGACCAGTGGAAACTTCTGCGTGATTTTGACGTCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0304721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0304721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RACE fragment cDNA #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRN; helicase; murine; diagnosis; RACE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to mRNA;
                                                                                                                                                                                                                      Score 81.2; DB 19;
Pred. No. 2.7e-13;
0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for diagnosis
                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                            Length 1164;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of human
                                                                                                                                                                                                                        ω,
                                                                                                                                                                                                                      Gaps
                      657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673
                                                                                                     597
                                                             568
                                                                                                                                            508
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AAV35115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                               Matches
                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                            This sequence encodes a novel mouse WRN helicase associated with Werner's syndrome. The mouse WRN the diagnosis of human Werner's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 22-23; 30pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-369863/32
P-PSDB; AAW59454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                       Sequence 4206 BP; 1284 A; 876 C; 976 G; 1070 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    New mouse gene encoding protein – used for diagnosis Werner's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP10146188-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Werner's syndrome; WRN; helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV35115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV35115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EIJI-) EIJIN KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse WRN helicase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp.
                                       541 TT---CATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAA
                                                                                                     481 GGAAGGTTGCGACTGTCCAGATATGTGTAAATTATTGTGATGTTATGCATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569
                                                                                                                                                      h 7.7%;
Similarity 52.9%;
98; Conservative
  CTTCCATGTCAGTTTTCCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGA
                                                                              GCAGAGTCGCAGTGATCCAGTTGTGTGTGTCTGAGAACAAATGTTACTTGTTTCACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA to mRNA; 4206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGATGCCTATGCT 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGATGCTTATGCT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGCTGCAGCAATTGGAGTAATTTCCCCCCTCACTGAGGACCAGAAACTGTATGCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCAGGGGTTGGGATTGAAGGGGGACCAGTGGAAACTTCTGCGTGATTTTGACGTCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGCCTCAATGGTCTGGTTAAACACGTCTTAGGGAAACAACTTTTGAAAGACAAGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0304721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96JP-0304721
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..4206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRN
                                                                                                                                                          Score 81.2; DB 19;
Pred: No. 5e-13;
0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine;
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protein which is gene is useful for

useful for

of,

Indels Length

ω,

Gaps

540

325

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RESULT 12
AAX83004
ID AAX83
XX AAX83004
XX AAX83
XX MUS
XX MUS
XX MUS
XX AAX83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
    Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                               This sequence represents the coding region for the mouse WRN gene. corresponding human gene (AAX83001) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disords a complex phenotype, as well as related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DARW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; WRN; Werner's syndrome; recessive disorder; phenotype;
                                                             Sequence 4792
                                                                                                                                                                                                                            Claim 1; Fig
                                                                                                                                                                                                                                                                      diseases
                                                                                                                                                                                                                                                                                          Isolated nu
useful for
                                                                                                                                                                                                                                                                                                                                                                                                              Fu Y, Mulligan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09724435-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse WRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX83004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX83004 standard; DNA; 4792 BP
    Local
                       Match
                                                                                                                                                                                                                                                                                                                                                 1997-363671/33.
DB; AAY14519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566
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  Similarity
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OSHIMA
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or detection a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGATGCCTATGCT 639
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                                                                                                                                                                                                                          6; 153pp;
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                                                             BP;
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95US-0580539.
96US-0010835.
96US-0594242.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                           1441 A; 1012 C; 1107 G;
                                                                                                                                                                                                                                                                                                                                                                                                              Oshima J,
  7.7%;
                                                                                                                                                                                                                                                                                     and treatment of Werner's s
                                                                                                                                                                                                                            English.
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                            Schellenberg
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  81.2;
No. 5.
DB 18;
.3e-13;
                                                             1226 T;
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                                                                                                                                                                                                                                                                                     syndrome, and
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                                                         6 other;
                   Length 4792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autosomal;
                                                                                                                        disorder
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                  Query Match
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                                                      This sequence encodes a novel mouse WRN helicase associated with Werner's syndrome. The mouse WRN the diagnosis of human Werner's syndrome.
                                                                                                                                             WPI; 1998-369863/32.
P-PSDB; AAW59454.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAV35114
                                      Sequence
                                                                                              Claim 3; Page 13-18;
                                                                                                                 New mouse gene encoding protein Werner's syndrome
                                                                                                                                                                                            15-NOV-1996;
                                                                                                                                                                                                                                   02-JUN-1998
                                                                                                                                                                                                                                                     JP10146188-A.
                                                                                                                                                                                                                                                                                                                                          Werner's
                                                                                                                                                                                                                                                                                                                                                           Mouse WRN helicase
                                                                                                                                                                                                                                                                                                                                                                               28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                 AAV35114;
                                                                                                                                                                          (EIJI-) EIJIN KENKYUSHO
                                                                                                                                                                                                                15-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCAAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAGCAAATGTTACTTGTTTCACATTTCTTCCATGTCAGTTTTCCCCCAGGGATTAAAA
                                                                                                                syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTTACTAGAAAAACAAATCAATTAAGAAGGCAGGGGTTGGGATTGAAGGGGACCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCCAA
                                                                                                                                                                                                                                                                                                                                          syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAAACAACTTTTGAAAGACAAGTCCATCCGCTGCAGCAATTGGAGTAATTTCCCCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                              (first
                                      BP; 1546 A; 1034 C; 1156 G;
                                                                                                                                                                                            96JP-0304721
                                                                                                                                                                                                                96JP-0304721
                                                                                                                                                                                                                                                                       /*tag= a
/product=
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          cDNA including non-coding
                                                                                                                                                                                                                                                                                                                                          WRN;
                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA
                                                                                                                                                                                                                                                                                                                                                                             entry)
         7.7%;
                                                                                              30pp; Japanese
                                                                                                                                                                                                                                                                                                                                          helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                    to mRNA;
                                                                                                                                                                                                                                                                         WRN
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Score 81.2; D
Pred. No. 5.4e
0; Mismatches
                                                                                                                                                                                                                                                                        helicase
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                                                                                                                          used
                                                                                                                                                                                                                                                                                                                                          murine;
                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                          for diagnosis of human
DB 19;
;.4e-13;
hes 173;
                                       1322
                                                                                                                                                                                                                                                                                                                                          diagnosis;
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gene is
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Best Local Similarity Matches 198; Conserv

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                                                                                                                                                                                                                                                                                                                                                                         12-APR-1996;
29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                                                                                                                                                                                                  Fu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9724435-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                    Claim 1; Fig 7; 153pp; English.
                                                                                                                                                      Isolated nucleic acid useful for detection a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recessive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; WRN; Werner's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial mouse
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                                                                                                                                                                                                                                                                                                             (DARW-) DARWIN
(OSHI/) OSHIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-1997
                                                                                                                                                                                                                       1997-363671/33
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                                                                                                                                                                                                                                                                Mulligan
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95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
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J.
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This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (AAX83004). The corresponding human gene (AAX83001) encodes a protein related to Werner's syndrome.

Sequences sequences

 $\tt ABB10981\hbox{-}ABB12330$ represent 1350 novel human polypeptides, and $\tt ABB08225\hbox{-}ABA09574$ represent nucleic acids encoding them. The

Claim 1; Page 436; 1963pp; English.

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; growth finamentopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antisthammatory; antistathiatic; antiarthritic; haemastatic; antiarteriosclerotic;
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                                                                                                                                                                  Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                       WPI; 2001-457740/49.
P-PSDB; ABB11264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000;
27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-)
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Pred. No. 0.0008;
""matches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC invention also relates to vectors and recombinant host cells comprising a CC antibodies against the polypeptides of producing the novel polypeptides, cc antibodies against the polypeptides of identifying compounds which CC bind to polypeptides of the invention. Although novel, many of the CC polypeptides of the invention have homology to known proteins, thereby CC giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention have homology to known proteins, thereby CC invential therapeutic applications. The polypeptides of the invention may CC differential therapeutic applications. The polypeptides of the invention may CC differential therapeutic probable biological activities, and hence CC themotractic or chemotinetic activity; itsue growth activity; CC immunomodulatory activity; activity or inhibit-related activities; chemotractic or chemotinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be conditions, e.g., and nucleotides of CC the invention are useful for preventing, treating or ameliorating medical CC conditions, e.g., because cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of CC the invention are useful for preventing, treating or ameliorating medical CC cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell caldsorders), chronic inflammatory conditions (e.g., asthma or arthritis), CC proliferative retinopathy, atherosclerosis, coronary heart disease, creativities and be used to promote wound the manufactions and incers), while those with immunomodulatory activities may be used to promote cell growth factor activity may be used to cell can be used to multiple to give rise to neuroepithelial cells chart can be used to neuroepithelial cells constituted to give rise to neuroepithelial cells constituted to give rise to neuroepithelial cells can only also be used to cell demanded to the diagnosis of 
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Best Local :
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                                                                                                                        TTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATC
                                                                                                                                                                                        TGCGGCAGAGAACAATTTGCTCTGTAATGGGCTTAGCCTGAAGTCCCTCGCTGAGACTG
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                                                                                                                                                                                                                                                                                                                                                                              ATATTTTGGCAGATGGCACCATTTTGAAAGTTGGAGTGGGATGCTCAGAAGATGCCAGCA
                                              CTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTT 864
                                                                                                                                                                                                                                                                                   AGCTTCTGCAGGATTATGGCCTCGTTGTTAGGGGGGTGCCTGGACCTCCGATACCTAGCCA 146
CTCTCACAGAGGACCAGGTAATTTATGCTGCCAGGGATGCCCAGATTTCAGTGGCTCTCT
                                                                                             TTTTGAACTTTCCCCTTGACAAGTCCCTTCTACTTCGTTGCAGCAACTGGGATGCTGAGA
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Search completed: June 14, 2003, 07:03:19
Job time: 322 secs

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Minimum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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ALIGNMENTS

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AUZ26180/c
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288.8 273.8 261 245 243.8 241.2

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site
           Unpublished (1999)
Other ESTs: AW460204 corresponding to Gm-c1015-3787 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
                                                               Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. an A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                    BE659005
GM700008A10G11 Gm-r1070
                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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/organism="Arabidopsis tl
/ob_xref="taxon:3702"
/clone="Ihb="RAFU14"
/clone_1tb="RAFU14"
/tissue_type="Toot"
/lab_host="DH10B"
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Fax: (217) 33-4582
Email: 1-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3225 FAX: (888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome ystems.com web site:www.genomesystems.com
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University of Illinois
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GTTGGAGCTGGGATTGATGGTGATGCTGTGAAGGTTTTTAGAGATTATAACATATCTGTT
                                                      GTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATC
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                                                                                                         ATTCATTCTGGAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAG
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//Clone_lib="Gm-r1070"
//Clone_lib="Gm-r1070"
//Clone_lib="Gm-r1070"
//Clone_r1be library Gm-r1070 is a sequence-driven, reracked
//Clones selected from cDNA libraries from
set of 9,216 clones selected from cDNA libraries from
various tissues and stages of development of soybean that
represent 2,639 sequences from immature cotyledons, 1,770
from young pods. The 5' ESTs of the source clones from
the different libraries was used to select singletons, or
a representative of each contig, which were reracked to
form library Gm-r1070. The cDNA clones of the reracked
Gm-r1070 library were then sequenced at the 3' end. The
contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Center for Computational
Genomics and Bloinformatics, University of Minnesota,
http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   information on the source library for each clone can
be obtained by referring to the Genome Systems clone
the original cDNA library that is also listed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reracking was performed by Genome Systems, St. Louis http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics,
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GA_Ea0013022f Gossypium_arboreum_7-10 dpa fiber library Gossypium
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Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 701.
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Clemson Universit
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,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm
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100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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                                                                                                                                                                                         Similarity
                   CAAATCAAATCCCCAATAATATCCGTCGCCAATTGCCTCGTTCCATCACTTCTACAT 264
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                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                       /cultivar="8400"
/db_xref="taxon:29729"
/db_nee="64_Ea0013022f"
/clone="64_Ea0013022f"
/clone_11b="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10"
                                                                                                                                                                                                                                                               /note="Vector: pBK-CMV; Site_1: 144 c 155 g 217 t
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                        'lab_host="E. coli"
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                                                                                                                                                                     Score 261; DB 12;
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                                 Contact: Shoemaker R/Public Soybean EST Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                               Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanne,A., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                               soybean.
Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
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                                                                                                                                                                                                                                                                                                (bases 1 to 552)
l: est@watson.wustl.edu
clone is available thr
through: ResGen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 bp
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                                                                                                                                                                                                                                                                                                                  TTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCCGGGGAAGG
TGACGGATCTTTCTTTTCATGCTAATCAAAAGCTTGGTGGAGATCATAAGTGGGGTCTTG
                                                                      CTGGGATTGATGGTGATGCTGTGAAGGTTTTTAGAGATTATAACATATCTGTTAAAGGTG
                                                                                             TTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATG
                                                                                                                                                                    TTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATT
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                                                                                                                                               CTGGAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAGGTTGGAG
                                                                                                                                                                                                                                                                                              CAATTGGATTTGACATTGAGTGGAAACCCCACCTTCAGAAAAGGTGTTCCTCCCGGAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anote—"Vector: pBluescript II SK; Site_1: EcoRI; Site_2: KNDI; This cDNA library was constructed from mRNA isolated from cotyledons of 3 - and 7 -day-old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthexix Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of stratagene's cDNA hemimethylated. A modification of stratagene's cDNA hemimethylated (V-A, C, or G) was added to the 3' end of the primer at the 5' end of the poly(A) tract. After second- strand synthesis, the cDNA ends were filled in with cloned pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhOI site within the first-strand synthesis primer was then restricted by digestion with XhOI; all XhOI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA size Fractionation column. The column eluent was then ligated vector (pBluescript II SK(+) that has been digested with EcoRI and XhOI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-30). This library was constructed by Dr. Paul Keim and Dr. Virginia 103 c 125 g 154 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GENOME SYSTEMS CLONE
/clone_lib="Gm-cl027"
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/db_xref="taxon:3847"
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Pred. No. 1.9e-50;
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AU237507
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                                                                                                                                                                                                                                                                                              171
                                                                                                                                                                                                     Conservative
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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana Eukaryota; Viridilplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1. (bases 1 to 671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibara
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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                                                                                             GACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGT----ATCAAAGATGTTGAGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCTTCTTGGTGTCTTTATCAGGCGATTAAAGATCTCCCGGACGC
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                                             ATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC 892
TTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAA
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/note="Site_1: BamH
'^a c 164 g
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/db_xref="taxon:3702"
/clone="RAFL16-31-E24"
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Pred. No. 3.8
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467 bp mRNA linear EST 03-DEC-2001 sm20bl1.y1 Gm-c1027 Glycine max cDnA clone GENOME SYSTEMS CLONE ID: Gm-c1027-9430 5' similar to SW:WRN_HUMAN Q14191 WERNER SYNDROME HELICASE. [1] ;, mRNA sequence.

AW832139

AW832139.1 GI:7926113
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High quality sequence stop: 417.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 734 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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314 286 1810
water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesix Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the liquide cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer [GACAGAGAGAGAGAGACTCTCGAG[7]18] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and
                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled which were propagated on paper towels with distilled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cotyledons of 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-9430"
/clone_lib="Gm-c1027"
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Abbal, P., Agasse, A., Ageorges, A., Atanasso Couture, C., Dedaldechamp, F., Delrot, S., GlHandi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                    BQ799068 661
EST 1237 Green Grape berries
CDNA Clone GT172E01 3', mRNA
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                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                              Vitis vinifera
                                                                                                                                                                                                                                                                           BQ799068
BQ799068.1
                                                                                                                                                                                                                                 Vitis vinifera.
                                                                                                                                         Vitaceae; Vitis
                                                                                                                    (bases 1 to 661)
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GI:22014034

Atanassova,R., Barrieu,F., ot,S., Glissant,D., Grimple

Grimplet, J.,

Grape Berry (skin, pulp

sequence. bp mRNA Lambda Zap

II Library

Vitis vinifera EST 30-JUL-2002

linear

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CTTCTTGGTGTCTNTATCAGGCGATTAAAGATCTCCCGGACGC
                                                                                                                                                                                                                                                              CACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGA 789
                                                                                                                                                                                                                                                                                                                                                                                                 AGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAGGTTGGAGCTG
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                                                     CTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC 892
                                                                                                             ATTGGGAGGCTCCTGTTTTGTCAAAGGAGCAACTAGAGTATGCTGCAACAGATGCTTTTG
                                                                                                                                                                                                                                                                                                                                           CGGATCTTTCTTTCATGCTAATCAAAAGCTTGGTGGAGATCATAAGTGGGGTCTTGCAT
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                                                                                                                                                                     ACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGGATGCTTATG 849
                                                                                                                                                                                                                              CTTTGACTGAAAAACTTCTATCAAAAACAGCTTAAAAAAGCCCAACAAAATAAGACTGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript(tm) II XR Predigested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-30). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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Pred. No. 1.6e-49;
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                                                                     BM406124
EST580451
end, mRNA
BM406124
   potato.
Solanum
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Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, E
Tel: 00-33-(0)4-99-61-28-52
Fax: 00-33-(0)4-99-61-28-57
                                                     BM406124.1
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                                                                                                                                                                                                                       GATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGCTGTC 896
                                                                                                                                                                                                                                                                                         AGGCTTGGGAACTGGGAGTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACG
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/cultivar="Shiraz"
/db_xref="taxon:29760"
/db_xref="taxon:29760"
/clone="ID="Green Grape berries Lambda Zap II Library"
/clone="ID="Green Stage"
/dev_stage="green stage"
/dev_stage="green stage"
/dev_stage="green stage"
/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco I; Site_2: XhoI; Oriented library, construction described in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier,N., Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158
(12): 1575-83 2001"
   tuberosum
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                                                                                 sequence.
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Best Local (
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                                                                  TIGGGGGATTGGGAGGCTAATGTGTTATCTAGGGACCAACTACATTATGCTGCTACAGAT
                                                                                                                                                                                                                      GATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAATTGGTGGAGATAAAAAATGGGGC
                                                                                                                                                                                                                                                                                           GGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAA
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GCCTTTGTTTCCTGGCACTTGTATCAGGCACTGAAGAGCCTTCCGGAGATTGT
                                                                                                   CTTGGGAACTGGGAGTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGGAT
                                                                                                                                     CTAGCATCACTAACCGAGAAGCTTCTTGCCAAGCAGCTCCCTAAGCCAAGCAATATCAGG
                                                                                                                                                                     CTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATCAGG
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                                 GCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGCTGT
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0;

Score 233.8; DB 13; Pred. No. 1.1e-47; Mismatches

Length

535; 0;

CM medium

187;

Gaps

0

534 895

481

421 782 361 722

301

662

241

602 181 121 482 61

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Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Research Genetics, Tel: 1-800-711-6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation of ESTs from potato roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanksley,S. and Baker,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Utterback, T., Chiemingo, A.,
/note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site
XhoI; supplier: Cornell University, Tanksley lab;
sequencing; The Institute for Genomic Research. Roots
isolated from in vitro grown stem cuttings on CM medi
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
a 101 c 136 g 152 t
                                                                                                                                                                                                                 /clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4113"
/clone="cPRO26F14"
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                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Kennebec
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Solanum tuberosum"
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ningo,A., Bougri,O., Buell,C.R., Ronning,C.,
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,C. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                  GAGAAATCTGCAGTAGAGCTGTTAAATTTTGTTGAGGAAAAGAAGAAGAAGAAGAAGGGAAT 61
GCTTTGGAAGATCTTTCCGAACTTGCCAACAAAAAGCTTGATGATCCCAAGAAGTGGAGT
                               GATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGGGC 722
                                                                GGTGTTTGCATTGCAAATGATGCTTTCAAAGTTCGCCAAGATCACAATGTATCTGTGAAG
                                                                                               GGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAA 662
                                                                                                                                 CACTCCGGAATCCCTCAAACTCTGCAATCTCTTGAGGATCCAACTGTTGTGAAGGTG
                                                                                                                                                                                                 AAGGCTGCTGTTATGCAGATATGTGGTGACAAGGGTAATTGTTATGTTTTGCATATCATC 181
                                                                                                                                                                                                                                                                    GTTGCTCTTGGATTTGACATTGAATGGAAGCCCACTTTTAGAAGAGGTGTGCCACCTGGG 121
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and Tanksley, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Four wk old greenhouse plants were stab inoculated on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr, Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen."

91 c 126 g 147 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato crown gall"
/tissue_type="crown gall"
/dev_stage="crown galls from full-grown plants (8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon
/cultivar="TA496"
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Pred. No. 5.6e-45;
0; Mismatches 175;
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Glycine max
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Public Soybean EST Project
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                                                                                                                                                                                                                                                                  /tissue_type="Leaf
old seedling"
                                                                                                                                                                                                                                                                                                                                 /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                               /clone_lib="Gm-c1066"
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                                                                                                                                                                                                                                                /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available through: ResGen, Invitro South Memorial Parkway Huntsville, AL 35801 For call: (800)-533-4363 or contact via email: ccu@r High quality sequence stop: 423.
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    164
                                                                                                                                                                                                                              /note="Noctor: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Noctor: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Noctor: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Noctor: pBluescript II SK+; Site_1: EcoRI; Short the condition of 2 week old seedling from the cultivar Williams The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were
                                                                                                                   directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library
                                                                                 was constructed in the laboratory of Dr. Randy
119 g
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301 For further information
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                                                                                                                                                              restriction site NA fragments were
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                                                                                                                                                                                                                                                                                                                                                                                BM358892 515 bp mRNA
GA_Ea0013P02r Gossypium arboreum 7-10 dp
arboreum cDNA clone GA_Ea0013P02r, mRNA
BM358892
                                                                                                         Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simme, D., Wood,T.C., Leslie,A. and Wilkins,T.A. An integrated analysis of the genetics, development, of the cotton fiber [Unpublished (2000)]
Email: rwing@clemson.edu
Total High Quality bases = 415
Seq primer: TAATAGACTACTATAGGG
High quality sequence stop: 514.
Location/Qualifiers
                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                                            864 656 7288
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277; Conserv
   Clemson |
                                           l (bases 1 to 517)

Ning,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                    אמיטטטטן 517 bp mRNA linear EST 09-JAN-200.
GA_Ea0013022r Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0013022r, mRNA sequence.
BM358891
                                                                                                                                                                                        Gossypium arboreum.
Gossypium arboreum
                                Contact: Wing RA
                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids_II; Malvales; Malvaceae; Gossypium.
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/note="Vector: pBK-CMV;
112 c 109 g 10
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/clone="GA_Ea0013P02r"
/clone_lib="Gossypium arboreum 7-10 dpa i/tissue_type="Fibers isolated from bolls
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/organism="Gossypium
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/cultivar="8400"
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Pred. No. 2.6e-32;
0; Mismatches 143;
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446

506

558

498

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438 266 378 206

326

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ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                         BM731125 555 bp mRNA linear EST 01-MAR-2002 sal68a05.yl Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4233 5' similar to TR:Q9SVM6 Q9SVM6 HYPOTHETICAL 35.1 KD
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Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 327
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 514.
   soybean
                                       BM731125.1
                                                           PROTEIN. ;, mRNA sequence.
BM731125
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
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Pred. No. 1.1e-31;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST I
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen
South Memorial Parkway Huntsville, AL 35801 For furt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                  CGCCAATTGCCTCGATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCGT
GTTCCTCCCGGAAAGGTAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTT
                                                                       GTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTT 530
                                                                                                             GAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGT 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBrL). This library was constructed in the laboratory of Dr. Randy Sheemaker."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="SOYBEAN CLONE ID: Gm-c1061-4233"
/clone_lib="Gm-c1061"
/tlssue_type="mature flowers of field grown plants"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                  176;
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CDNA clone wh21m08 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 595)
Ogihara, Y. and Murai, K.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Y. Ogihara unpublished cDNA library,
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh21m08"
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Pred. No. 9.1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanceae; Solanum.

1 (bases 1 to 499)

1 (bases 1 to 499)

Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chlemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPCAZ86 5
BI433038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 bp mRNA line EST535799 P. infestans-challenged leaf Solanum PPCAR86 5' sequence, mRNA secuence
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
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EST.
                                                                                                                                                                                                                                                                                                                                                                    For clone info: please contact Division tel 1-800-711-6195, em
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCTTTACAAGGT 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCAAGGAAAATGTTCAATGATTATGATGTCCGTGTACAACCATTGATGGATTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAAGGTATTGGATTGATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGAGTGGAAACCCTTTCCCAGAAGAGGAGAACCACCATGTAAAGTCGCGTTGATGCAA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGTACGCAAAATCGAAAGCATGA---AGGCCTCTGGCCCGGTCTCCCTTGGTTTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTTTGTTCTCTCAAAAAAGCAACTTGAGTATGCTGCTACCGATGCCTACATCTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer: M13F-R.
/note-"vector: pBluescript SK(-); Site_1: EcoRI; XhoI; Whole plants were challenged with 450,000 sporangia,ml P. infestans US-1(US 940501) in BtG (Madison, Wisconsin). Leaf tissue was collected
                                                                                             /clone_lib="P. infestans-challenged
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
                                                                                                                                                                                             /db_xref="taxon:4113"
/clone="PPCAZ86"
                                                                                                                                                                                                                                                /cultivar-"Kennebec
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                         /organism="Solanum
                                                                                                                                                                                                                                                                         tuberosum"
                                                                                                                                                                                                                                                                                                                                                                       email
                                                                                                                                                                                                                                                                                                                                                                                              Research Genetics, Libraries
                                                                                                                                                                                                                                                                                                                                                                       cdna@resgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
     501) in Biotron collected at 1
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                                                                         EcoRI; Site_2:
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521

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281

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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 245; Conserv
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                  656 TATCAAAGATGTTGAGGATCTTTCAGATTTTAG 687
                                                                                         596 AAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           296 AGCTAGGAATTITCCAGCAATGAGGTTTGGTAGGATTTTTGTATAGCAAGACTGCTAC 355
                                                                                                                                    CCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCA 535
                                                                                                                                                                                                                                                                               TGTGAAGGCTTTGGAAGATCTTTCTGAACTTG 499
                                                                  GAAGGTGGGTGTTTGCATTGCAAATGATGCTTACAAAGTTCGCCAAGATCACAATGTATC 467
                                                                                                                                                                                                      TGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCT 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 156.8; DB 13; Length 499; 62.5%; Pred. No. 1.8e-28; Vative 0; Mismatches 147; Indels 0; Gaps
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Search completed: June 14, 2003, 08:23:16 Job time: 1830 secs

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Maximum DB
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     seq length: 0 seq length: 2000000000
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                              Issued_Patents_NA: *
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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6 5208

6 6476

7 98844

3 98844

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US-09-791-211-11
US-09-127-670-5
US-08-781-891-205
US-08-781-891-207
US-08-781-891-207
US-08-781-891-207
US-08-791-211-10
US-08-791-21-10
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US-09-416-213-1
US-09-426-290-1
US-08-623-906A-1
US-08-961-527-177
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4730.940 Million cell updates/sec
                                     Sequence 70, Appl
Sequence 11, Appl
Sequence 205, Appli
Sequence 207, App
Sequence 207, Appl
Sequence 14, Appl
Sequence 1, Appli
Sequence 2258, Appli
Sequence 762, Appli
Sequence 71, Appli
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; Patent No.
; GENERAL IN
396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTTGGCTTGGATATTGAGTGGAGACCA
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3.1 1946 3 US-08-3 3.1 1946 4 US-08-3 3.1 1185 1 US-08-3 3.1 1185 1 US-08-3 3.1 1185 1 US-08-3 3.1 1185 1 US-08-3 3.1 1185 4 US-09-3 3.1 1846 3 US-09-3	32.24 3.1 1956 4 US-08-76-76-76-76-76-76-76-76-76-76-76-76-76-	a						C								a	O		
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		US-08-334-254-7	-023	US-08-370-975B-1	US-08-370-975B-6	US-09-420-915-15	US-09-173-581-15	US-09-149-476-116	PCT-US92-03624-9	US-09-222-594-9	US-09-076-137-9	US-08-904-278-9	US-08-316-301A-9	US-08-049-783-5	US-07-876-280-8	US-09-448-894-140		US-08-559-896B-1	907-TKQ-TQ/-90-SD

ALIGNMENTS

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT IMFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TTELEPHONE: (206) 622-4900
Query Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                      TELEPHONE: (206) 622-
TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and STREET: 6300 Column CITY: Seattle STATE: Washington
                                                                                                                      LENGTH: 5208 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 98104-7092
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6300 Columbia Center, 701 Fifth Avenue
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Yu, Chang-En
Oshima, Junko
Mulligan, John T.
    Conservative
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  Score 111; DB 3; Length 52
Pred. No. 2.5e-25;
0; Mismatches 225; Indels
                                            Length 5208;
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; LOCATION: (232)...(4530)
US-09-791-211-11
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US-09-791-211-11
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APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION
FILE REFERENCE: RTS-0205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09791211 Patent No. 6448080
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5208
TYPE: DNA
ORGANISM: Homo s
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 11
                                                                                                         493
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     CTTATTGAAGATTCAACACTTGTAAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG
                                                         AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCCTCAAAGTCTCCCAACAT
                                                                                                                         AGTTTTAGAAAAGGTGTTCCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT
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                                    AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCCAGGGATTAAAAAATG
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Pred. No. 2.5e-25;
0; Mismatches 225;
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, NAME/KEY: CDS
; LOCATION: (229)...(4432)
US-09-127-670-5
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US-09-127-670-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09127670 Patent No. 6228583
                                                                                                                                                                                                                                                                                                                            Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ASSAYS FOR COMPOUNDS WHICH EXTEND TITLE OF INVENTION: SPAN FILE REFERENCE: MIT-7720pA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Massachusetts Institute
APPLICANT: Leonard P. Guarente
APPLICANT: David A. Sinclair
APPLICANT: David B. Lombard
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 6476
TYPE: DNA
ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/127,670 CURRENT FILING DATE: 1998-07-31 EARLIER APPLICATION NUMBER: US 60/054,629 EARLIER FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                            Match 7.9%;
Local Similarity 53.2%;
                   718
                                                                                                                     614
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                                                                                                                                                                                      554 CTTCCATGTCAGTTTTCCCCCCAGGGATTAAAAATGTTACTAGAAAACAAATCAATTAAGA 613
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GGGGCCTTGCCTCACCTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAA 777
                                                                    TCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAAT 717
                                                                                                                                                                                                                                                           GCAGAGTCGCAGTGATCCAGTTGTGTGTGTCTGAGAACAAATGTTACTTGTTTCACATTT
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                                                    TGGAGAGTTTTGTGGAGCTGACGGATGTTGCCAATGAAAAGTTGAAGTGCGCAGAGACCT 733
                                                                                                                     AGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTA 657
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                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                          Score 82.8; DB 4;
Pred. No. 3.7e-16;
                                                                                                                                                                                                                                                                                                                            Mismatches 172;
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US-08-781-891-205
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SEQUENCE CHARACTERISTICS:
LENGTH: 4792 has
                                                                                                                                                                                                           Matches 179;
                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Fu, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
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                                                                                                                                                                                                                           Local
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     562
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5. 6090620
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                                                                                                                                                                                                                           Similarity
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                                                                                      CATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTG
 AAACTTCTGCGTGATTTTGACGTCAAGTTGGAGAGTTTTGTGGAGCTGACGGATGTTGCC
                               AAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCC 689
                                                                   ATGTTACTAGAAAACAAATCAATTAAGAAGGCAGGGGTTGGGATTGAAGGGGACCAGTGG
                                                                                                                                    GAGAGCAAATGTTACTTGTTTCACATTTCCTTCCATGTCAGTTTTCCCCCCAGGGATTAAAA
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52.3%;
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Mismatches 1
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US-09-791-211-10
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                                                                                                                                                                                                         Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
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APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: unknown
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 45541
                                                                                                                                  45421 TACAGTTTTTCCCCCAGGGATTAAAAATGTTGCTTGAAAATAAAGCAGTTAAAAAGGCAGG
                                                                                        605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA
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TTTTGTGGAGTTGACAGATGTTGCCAATAAAAA 45573
                               TGTTGAGGATCTTTCAGATTTAGCCAACCAAAA 697
                                                                 TGTAGGAATTGAAGGAGATCAGTGGAAACTTCTACGTGACTTTGATATCAAATTGAAGAA 45540
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                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                      Score 55.4; DB 4;
Pred. No. 1.4e-06;
0; Mismatches 61;
                                                                                                                                                                                                                                     Length 98844;
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US-08-232-463-14
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US-08-781-891-207
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                                                                                                                   Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
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Best Local :
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
APPLICANT: DORNEK, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
TITLE OF SPOIENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 29604 base pai
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NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                            .665 TGTTGAGGATCTTTCAGATTTAGCCAAACCAAAAAATTGGTGGAGATAA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                         545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG
                                                                                                                                                                                                                                                                                                                                                                   605 TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.98;
Similarity 56.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
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Yu, Chang-En
Oshima, Junko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51.2; DB 3; Pred. No. 1.5e-05;
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RESULT 8 US-09-300-672-3

Sequence 3, Application US/09300672 Patent No. 6248937

GENERAL INFORMATION:
APPLICANT: Finkelstein, Ruth R.
APPLICANT: Lynch, Tim
APPLICANT: Goodman, Howard M.
APPLICANT: Wang, Ming-Li

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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TELEX: 899149
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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1112
                                                                                                                                                                                     249 ATCACTTCTTACATCTTATAAACGATTTCCTCTCTCCCGTTGCC 294
                                                                                         189 GGCCACGAGGAGGATCCAAATCAAATCCCCAATAATATCCGTCGCCAATTGCCTCGTTCC 248
                                                                                                                                                      129 CGTTCTTCTTCTTCCTCTCTCCTCTGCTGCTCCGACCGTACAAGCTACAACCTCCGTCCAT 188
                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                          ch 4.7%;
1 Similarity 11.5%;
33; Conservative 14
                                                                                                                                                                                                                                                                             9 ATTAATTTTTATTTTTTTTTTCAGTAAAAGAAATGTCATCGTCAAATTGGATCGACGAC
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                                                                                                                       GCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAATTTCTCC 128
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.8e-05;
0; Mismatches 113;
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                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (151)..(1134)
US-09-300-672-1
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                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1500
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Patent No. 6248937
                                                                                                                                                                                                                 Matches
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Best Local (
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LENGTH: 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Finkelstein, Ruth R.
APPLICANT: Lynch, Tim
APPLICANT: Goodman, Howard M.
APPLICANT: Wang, Ming-Li
TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480.89(HY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/300,672 CURRENT FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT, TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE FILE REFERENCE: 480.89(HV)

CURRENT APPLICATION: NUMBER: US/09/300,672

CURRENT FILING DATE: 199-04-27

NUMBER OF SEQ ID NOS: 16

NUMBER OF SEQ ID NOS: 16

SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis FEATURE:
                                                                       164
                                                                                                   172 CTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCCAATAATACCGTC
                                                                                                                                        104 CTCTCTACTTCCTCTTCTTCTTCTTCTTCTTCATCTATGGACCCTTTAG
                                                                                                                                                                          112 CTTCCTACAATTTCTCCCGTTCTTCTTCTTCTTCTTCCTGCTGCTGCTCCGACCGTACAAG
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224 CTCAATCCGATTCCACCACCGACTCATCAACTTCCT 259
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                                                                                                                                                                                                             ch 3.7%;
l Similarity 53.2%;
83; Conservative
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                                 GCCAATTGCCTCGTTCCATCACCTTCTACATCTT 267
                                                                   CTTCCCAACATCAACACCATCTGGAAGATAATAACCAAACCCTAACCCATAATAATC
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Pred. No. 0.017;
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                                                                                                                                                                                                                                               DB 4; Length 1500;
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RESULT 10

RESULT 11 US-08-485-216-1

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                              Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Breen, John P
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                           3032
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                                                                                                                                                                                                                                                                                 434 CTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGAC 493
                                                                                                                                                                                                                                                                                                                  126;
                                                                                                                                                                                                                                                                                                                               Similarity
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TAATCAAAATATTAATCTCGTAAAACTTGATGAA 3185
                             TCTTTCAGATTTAGCCAACCAAAAAATTGGTGGA 707
                                                                                          TGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGA 673
                                                                                                                           TTCGAGTAATTTGTATAATGCTAAAAGGAGAATGTTATTATATAAATGAAAAACCTAATTG
                                                                                                                                                       TTTACAGAGAACTGAAAAAAAAAAATTATTGGGGTGTGTGGGTTGCAAGTGAATCTGTTAA 3031
                                                                                                                                                                                                          TGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTAT 553
                                                            TGTTATTGACAAAGTAAATCATTTCTCATTTACTTCCCTCACAACAAATGATATTGATTT 3151
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Kappe, Stefan
                                                                                                                                                                                                                                                                                                                  Conservative
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RESULT 12
US-09-003-245-1
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                                          Sequence 1, Applic Patent No. 5981189
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Best Local
 GENERAL INFORMATION:
APPLICANT: Chan, 1
APPLICANT: Han1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612/332-9081
INFORMATION FOR SEQ ID NO: 1:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chan, Voon APPLICANT: Hani, Eric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO 9. FILING DATE: 13-MAY-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                       689 CAACCAAAAATTGGTGGAGATAAAAA 715
                                                                                                                                                                                                                                                                                                               509 AGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCA 568
                                                                                                                                                                                                                                                         858 TGTTGATCCCCAAAATTCAGCAGTTGTAAGCATAGGAGCTTTTAATGCTGGACATGCTTT
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5, 5695960
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                                                       Application US/09003245
                                                                                                                           TAGAAAGCTAACTGAAGAAAAAAAAA 1004
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3100 No. 5695960west Center,
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Chan,
Hani,
                                                                                                                                                                                                                                                                                                                                                        Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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 Voon
Eric
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Pred. No. 0.
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RESULT 13
US-08-853-552-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Mueller, Douglas
REGISTRATION NUMBER: 30,
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MEDIUM TYPE: Floppy disk
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3100 No. 5981189west Center, 90 South Seventh Street
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47.8%;
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Sequence 1, Application Patent No. 6013501
GENERAL INFORMATION:
APPLICANT: Chan,

Application

US/08853552

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RESULT 14
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; LOCATION:
US-08-853-552-1
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                                                                               GENERAL INFORMATION:
APPLICANT: Allen, Steve
                                                                                                               Sequence 3, Application US/09346408B Patent No. 6338966
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Best Local Similarity
APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation
FILE REFERENCE: BB-1167-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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LENGTH: 1338 base pairs
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: 7933.29US02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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612/332-9081
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ilarity 47.8%;
Conservative
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Pred. No. 0
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-762
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LENGTH: 1272
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LENGTH: 2280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/992,833
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Momordica charantia
                                                                                                                                                                                                                                                                                                                                                                                                           Match 3.2%; Local Similarity 50.7%;
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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:/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
:/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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10 US-09-864-761-20174
10 US-09-864-761-20174
10 US-09-884-761-71
10 US-09-884-6503
10 US-10-131-061-71
10 US-10-131-061-71
10 US-09-186-095-3
10 US-09-186-095-3
10 US-09-464-767-1
10 US-09-464-767-3
10 US-09-464-767-1
10 US-09-464-767-1
10 US-09-464-767-3
10 US-09-754-853A-1
10 US-09-937-971-3
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Compugen
Sequence 31, Appl
Sequence 1131, App
Sequence 127, App
Sequence 220, App
Sequence 20174, A
Sequence 4570, Appl
Sequence 71, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 20, Appl
Sequence 1, Appli
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APPLICANT: Brown, Joseph P.
APPLICANT: LifeSpan BioSciences, Inc.
TITLE OF INVENTION: Nucleic Acid Sequences and TITLE OF INVENTION: Associated With Aging FILE REFERENCE: 017473-0011110US
CURRENT APPLICATION NUMBER: US/09/292,758
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: US 60/081,887
EARLIER APPLICATION NUMBER: US 60/081,887
EARLIER FILING DATE: 1998-04-15

WITHOUT OF SEO ID NOS: 147
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Best Local Similarity 54.1%;
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                             SEQ ID NO 31
LENGTH: 5189
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTTTTTGGCTTTGGATATTGAGTTGGAGACCA 455
                                                                                                                                                               433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA
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     TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA
                  CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG
                                                       AGCAPATGTTACTTCCACGTTTCTTCCATGTCAGTTTTTCCCCCAGGGATTAAAAATG
                                                                                  AATTATTGTGATGTTATGCATATTTTT----CATTCTGGTATCCCTCAAAGTCTCCAACAT
                                                                                                            TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTTTTCTGAG
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US-09-818-945-1860

US-09-818-945-247-30

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US-10-175-523-184

0 US-9-864-761-8619

US-10-184-644-458

US-10-184-644-458

US-09-770-445-860
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Pred. No. 2e-21; 
0; Mismatches 225; Indels
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Sequence 605, Ap
Sequence 270, App
Sequence 184, App
Sequence 184, App
Sequence 458, App
Sequence 458, App
Sequence 458, Appli
Sequence 3, Appli
Sequence 7317, Ap
Sequence 7317, Ap
Sequence 1860, Ap
Sequence 1860, Ap
Sequence 4759, Ap
Sequence 4759, Ap
Sequence 4754, Ap
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Sequence 8015, Ap
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Sequence 57, Appl
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; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-954-456-1131
; Sequence 1131, Application US/09954456
; Patent No. US20020115057A1
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                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1131
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin vor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 689290-76
                                                                                                                                                                                          Local
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FILLING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,711
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/60/235,720 ETILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,840 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/60/235,637 FILING DATE: 2000-09-26
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                                                                                              433
                                                                                                                 396 GATACCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 455
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                   TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTGTTTCTGAG
                                                       AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCCGACTGTCCAGATATGTGTAGATAGT 515
                                                                                              GATATTAGCATGAGTCTATCAGATGGGGGATGTGGGGATTTGACATGGAGTGGCCACCA
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                        10.6%;
                                                                                                                                                                 Score 111; DB 1
Pred. No. 2e-21;
0; Mismatches 2
                                                                                                                                                                                                        DB 10;
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US-09-729-674-127
"~quence 127, Ar
                                                                                                                                                                                                                       ; SEQ ID NO 127
; LENGTH: 3149
; TYPE: DNA
; ORGANISM: Homo saplens
US-09-729-674-127
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GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                    Matches
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APPLICANT:
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PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEC. 70.000-03-30
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 283 SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
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                                                                                                                                                                     Local Similarity
                                  631 AGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCCA 690
                                                                                                                                                    148;
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                                                                                              ATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGA 630
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LaVallie, Edward R.
Collins-Racie, Lisa !
Evans, Cheryl
                                                                       ATATTTTGGCAGATGGCACCATTTTGAAAGTTGGAGTGGGATGCTCAGAAGATGCCAGCA 529
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AGCTTCTGCAGGATTATGGCCTCGTTGTTAGGGGGTGCCTGGACCTCCGATACCTAGCCA
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Spaulding, Vikki
Wong, Gordon G.
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Treacy, Maurice
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                                                                                                                                                    Conservative
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Pred. No. 0.045;
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US-10-123-155-464/c ; Sequence 464, Application US/10123155 ; Publication No. US20030068794A1
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Best Local Similarity
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NUMBER OF SEQ ID NOS:
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APPLICANT:
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CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30
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TYPE: PRT
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                    TADACM..CA.SHWCHH.RDB.RRCNKCBN.M.W.B.....BHAMAM...YDBKNSMSA
                                                                                             YM.K.MRK...N.C.B.K.A.DM.R.S.H.TM.S.MC.SB...TNN..STYHNSSB
                                                                                                                                      CATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCCGTTGCCGAGCTAGGAATTT 307
                                                                                                                                                                           RC.TY.BG..RNDBGT....SY.K..SBSC.HAWA.MH..HY..Y...TM..A.B.NKH
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                             3.9%; Score 41.4; DB 9; 7.7%; Pred. No. 0.15; tive 215; Mismatches 476;
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US-08-781-986A-220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 220, Application US/08781986A Publication No. US20030054436A1
                                                                         REFERENCE/DOCKET NUMBER: PBS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8510
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles TITLE OF INVENTION:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: HP Vectra
OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
STRANDEDNESS:
TOPOLOGY: lir
                                      TYPE:
                                                                                                                                                                                           NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9410 Key West Avenue
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linear
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                      double
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US-09-864-761-20174/c

: Sequence 20174, Application

: Patent No. US20020048763A1
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                    PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                     SOFTWARE: Annomax Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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NO 20174
TH: 439
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FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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                                                                                                                                                       APPLICATION NUMBER: UFILING DATE: 2000-09-
                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
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Chen, Wensheng
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Pred. No. 1
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                                                            GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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US-09-938-842A-4570/c
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                           NUMBER OF SEQ ID
SEQ ID NO 4570
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4570, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 163;
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Local Similarity 43.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTGGTGATGATGGTGATGCTGCTGATGGTGTTGATGGCGATGCTGATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAGAGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAACGATGATGCTGATGGTGATGATAATGATGGTGATGCTACTGCTGTTGCCACTGATG
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ON: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

ON: EXPRESSED IN HELA, SIGNAL = 1.2

ON: EXPRESSED IN HELA, SIGNAL = 1.4

ON: EXPRESSED IN BRAIN, SIGNAL = 1.4

ON: EXPRESSED IN BRAIN, SIGNAL = 1.5

ON: EXPRESSED IN PLACENTA, SIGNAL = 1.5

ON: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

ON: EXPRESSED IN BEART, SIGNAL = 1.5

ON: EXPRESSED IN BT474, SIGNAL = 1.5

ON: EXPRESSED IN ETTAL LIVER, SIGNAL = 1.5

ON: EXPRESSED IN ETTAL LIVER, SIGNAL = 1.5
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Pred. No. 0.8;
0; Mismatches
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639 135 579 195

TRANSGENIC

PLANTS CONTAINING

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GENERAL INFORMATION:

APPLICANT: Lassner, Michael
APPLICANT: Metz, James G
APPLICANT: Metz, James G
APPLICANT: Facciotti, Daniel
TITLE OF INVENTION: SCHIZOCHYTRIUM PKS GENES
FILE REFERENCE: CGNE.131.02US
CURRENT APPLICATION NUMBER: US/10/331,061
CURRENT FILING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: US/09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/048,650
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR APPLICATION NUMBER: 09/99,793
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin Ver. 2.0
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; ORGANISM: Schizochytrium aggregatum
US-10-331-061-71
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US-10-124-800-3
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                                                                                                                                                                                                                                                                     Sequence 3, Application US/10124800 Publication No. US20020194641A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 71
LENGTH: 5215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 71, Application US/10331061 Publication No. US20030101486A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                        APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: PUFA POlyketide Synthase
FILE REFERENCE: 2997-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                    CURRENT APPLICATION NUMBER: US/10/124,800 CURRENT FILING DATE: 2002-04-16
            PRIOR APPLICATION NUMBER: 09/231,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 TTCTTCCTCTGCTGCTCCGACCGTACAAGCTACAACCTCCGTCCA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 TTCTCCCGTTCTTCTTCT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       653 CAAACCATTGGATTACATTTTTTTGTTCGTGTAGAAGTTAATCAGGCGGCTAGTTGACTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 AGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAATTTCTCCCCGTTCTTCTTC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTTCTTCTTCTCCGTCGCCTGCTCCTTCGGCCCCCGTGCA 3273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTGCTTTCTTTTTTTTTTT 513
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Pred. No.
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Pred. No. 16;
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                                                                                                                         Systems and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6503
**FWORTH: 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US200 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6503, Application US/10198846 Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/323,269 PRIOR FILING DATE: 2001-09-18
                                                                                                                                        FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: 701, 743, 884, 921, 931, 993, LOCATION: 1202, 1217, 1233, 1260, 1295, LOCATION: 1418, 1448, 1459, 1465, 1494, 1653, 1665, 1670,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-01-14
                                                                                                                                                                                                                                                                                                                      LOCATION: 3, 6, 7, 8, 20, 24, 33, 48, 83
LOCATION: 106, 108, 110, 112, 114, 116,
LOCATION: 130, 132, 134, 136, 138, 148,
LOCATION: 185, 217, 221, 234, 243, 330,
OTHER INFORMATION: n - A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (1)..(6177)
OTHER INFORMATION:
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NAME/KEY: misc_feature
LOCATION: 1753, 1774, 1785,
LOCATION: 1834, 1843, 1856,
                                                                                                                      LOCATION: 1621, 1635, 1653, :
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 3, 6, 7, 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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FILING DATE: 2001-04-16
APPLICATION NUMBER: 60/298,796
FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 AGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAATTTCTCCCCGTTCTTCTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6177
                                                                                                                   1202, 1217, 1233, 1260,
1418, 1448, 1459, 1465,
1621, 1635, 1653, 1665,
DRMATION: n = A,T,C or G
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59.0%;
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1867
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Pred. No. 18
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4, 116, 118, 1
8, 148, 149, 1
3, 330, 389, 4
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1312, 1316,
1501, 1518,
1688, 1710,
                                 1808,
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                                 1818,
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122, 124, 126, 1
152, 159, 171, 1
456, 536, 644
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1331,
1549,
1721,
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                                 1823, 1827, 1829
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Gaps

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A,T,C ဝင္ပ

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SEQ ID NO 3

LENGTH: 99916

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(99916)

OTHER INFORMATION: n = A,T,C or G
US-09-816-095-3
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US-09-816-095-3/c
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 120; Conserv
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APPLICANT: GAN, Weiniu
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOO1147 CURRENT APPLICATION NUMBER: US/09/816,095 CURRENT FILLING DATE: 2001-03-26 NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                    41589
                                                                                                                                                                                                                                           41649 TTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACTAGCTCCTCTTTGTGCCCCTGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                  TGCCTCAATTTCAGAAGCTGTCACTGAACTATTTAGAGATTCAACTTCTTCCTGGTTTAG
                                                                                                                                       TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG
                                                                                                                                                                                AGCAGCAGTT 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGTAGAGGTGTTTATAGT 41390
                           TGTTGAGGATCTTTCAGATT 684
                                                         TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
                                                                                                                                                                                                             GGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCA 544
                                                                                                                                                                                                                                                                           TTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGGGGAA
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    Mismatches

                                                                                                                                                                                                                                                                                                      Score 36; DB 10; Length 99916;
Pred. No. 1.3e+02;
0; Mismatches 140; Indels 0
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Pred. No. 9
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9.2;
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                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                      Gaps
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Matches

81;

Conservative

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4e+02;

95;

Indels

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Gaps

0

112 CTTCCTACAATTTCTCCCGTTCTTCTTCTTCTTCTTCTTCCTCCTGCTCCGACCGTACAAG 171

172 CTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCCAATAATATCCGTC

231 391018

390956

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; NAME/KEY: misc_feature
; OTHER INFORMATION: n i:
US-09-771-208-20
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            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROV
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILLING DATE: 2001-01-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
LOCATION: (494715)..(494814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/999,477 PRIOR FILING DATE: 1997-12-29
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                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (183872)..(183891)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified
                                                                                             LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (390986)..(391005)
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OTHER INFORMATION: n is unidentified
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                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                     LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n is unidentified
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LOCATION: (317174)..(317193)
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: n is unidentified
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LOCATION: (346860)..(346823)
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            3.4%;
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Score 36; DB
Pred. No. 4e+0
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                                                                                                                                                                                                   ; SOFTWARE: PatentIn version 3.0; SEQ ID NO 3; LENGTH: 32745; TYPE: DNA; ORGANISH: synthetic construct US-09-464-767-3
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US-09-464-767-3
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; TYPE: DNA
; ORGANIEM: Ovine adenovirus
US-09-464-767-1
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US-09-464-767-1
                                                                                                                                Query Match 3.4%;
Best Local Similarity 50.9%;
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09464767 Patent No. US20020045249A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Both, Gerald
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                                                                                                                                                                                                                                                                                                   APPLICANT: Boyle, David
APPLICANT: Vrati, Sudhanshu
TITLE OF INVENTION: DNA Encoding Ovine Adenovirus
FILE REFERENCE: 50179-073
CURRENT APPLICATION NUMBER: US/09/464,767
CURRENT FILING DATE: 1999-12-16
RUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/464,767
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boyle, David
APPLICANT: Variati, Sudhanshu
TITLE OF INVENTION: DNA Encoding Ovine Adenovirus (OAV287) and Its Use as a Viral Ver
FILE REFERENCE: 50179-073
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Both,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 3.4%;
Local Similarity 50.9%;
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                                                            6587 TIGATICAAGACCATGATTITCACAAAACGTTGACCAGTATTTTTTAGCTACTGAAATTT
6707 TTACAAAACATTCTCTGTTTACCTCATAACCTATATCGGTAGCTATT 6753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 TTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGA 501
                 502 TATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 TATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAA 561
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gerald
                                                                                                                                Score 35.8; DB 10;
Pred. No. 70;
0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                    (OAV287) and Its Use
                                                                                                                                 Indels
                                                                                                                                                               Length 32745;
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Search completed: June 14, 2003, 09:31:29 Job time: 225 secs
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US-09-754-853A-1
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.9
---- 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 127197
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09754853A Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                      18164 AATAAATTGAAGTTTATCAAAACCAATGCTTTCGGCTTCTGAAAT 18208
                                                                                                                                                         18104 TATCAAAAACTTATTATTTTTTTTAGGACGAGGAAGGTGCTGTAAATGAAAAGGAAGT 18163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6706 TTACAAAACATTCTCTGTTTACCTCATAACCTATATCGGTAGCTATT 6752
                                                                                                                                                                                                                                                             501 ATAIGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGAT 665
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                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                             Score 35.4; DB 9;
Pred. No. 2.2e+02;
0; Mismatches 81;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
24791104 seqs, 12571243825 residues
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/cgn2_6/ptodata/1/pna/US08_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/pna/US06_COMB.seq:*
/cgn2_6/ptodata/1/pna/US07_COMB.seq:*
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48: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:  
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79: /cgn2_6/ptodata/1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

17 18 19 20 21	c 166 100 111 111 111 111 111 111 111 111	C C 5 4 4 3 2 1	Result
142.4 142.4 142.4 142.4 142.4	276.2 276.2 181.2 174.8 174.8 174.8 174.8	1049 1039 1002.2 831 831 831 471.6 302.2 302.2	Score
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17 17 37 56 20	32 32 32 31	33 19 19 28 33 33 24	DB
US-09-391-146A-21024 US-09-371-146A-210624 US-09-985-678-210624 US-60-125-818-10555 US-09-534-859-326	US-09-906-226-15 US-09-605-698-9441 US-09-605-698-9441 US-09-849-529A-2068 US-00-196-868-2068 US-09-708-427-65909 US-09-708-427-83271 US-09-908-736-1476	US-09-896-186B-23 US-09-513-996A-67235 US-09-513-996A-28855 US-09-708-427-27137 US-09-896-186B-1 US-09-620-393B-6112 US-09-534-859-579 US-09-833-736-579	ID
Sequence 210524, Sequence 210524, Sequence 210524, Sequence 10555, A Sequence 326, App		Sequence 23, Appl Sequence 67235, A Sequence 28855, A Sequence 27137, A Sequence 1, Appli Sequence 579, App Sequence 579, App	Description

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Sequence 23, Application US/09896186B
GENERAL INFORMATION:
APPLICANT: Joshua Z. Levin
APPLICANT: Ken Philips
APPLICANT: Greg Budziszewski
APPLICANT: Fred Meins
CURRENT FILENGE: PB/5-31481A
CURRENT APPLICATION UNUBER: US/09/896,186B
CURRENT FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 1049
                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Arabidopsis US-09-896-1868-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-896-186B-23
                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 1049
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 CTCGTTCCATCACTTCTACATCTTATAAACGATTTCCTCTCTCCCGTTGCCGAGCTA
                                              CCGTCCATGGCCACGAGGAGGATCCAAATCCACATAATATCCGTCGCCAATTGC
                                                                                                                                                                                               ACCAAAGCATTAATTTTTATTTTTTGTTTCAGTAAAAGAAATGTCATCGTCAAATTGGA
                                                                                                TCGACGACGCTTTTACAGAGGAAGAGCTTCTCGCCTATCGACGCCATCGAAGCTTCCTACA
                                                                                                                                                  TCGACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACA
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ilarity 100.0%;
Conservative
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US-09-263-191-14639

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US-09-371-146A-155805

US-09-955-7254-113-155805

US-09-654-617-30344

7 US-09-654-617-16008

7 US-09-684-016-30344

5 US-09-654-617-16008

7 US-09-684-016-30344

5 US-09-684-016-30344

1 US-09-684-016-3044

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1 US-09-819-091A-3796

1 US-09-819-01A-3796

1 US-09-819-01A-3796

1 US-09-819-01A-3796

1 US-09-819-01A-3796

1 US-09-819-01A-3796

1 US-09-186B-17

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1 US-09-186B-1176

1 US-09-186B-1176
                                                                                                                                                                                                                                                  0;
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Pred. No. 5.8e-286;
Mismatches 0;
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                                                                                                                                                                                                                                                                         Length
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                                Sequence 67235, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRATIFLE OF INVENTION: SEQUENCE-DETERMINED DNA FRATIFLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 2750-709p
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 67235
LENGTH: 1114
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE: INVENTICE
ENTRY OF THE SECOND OF THE SECOND OF THE SECOND ORGANISM: Arabidopsis thaliana
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US-09-513-996A-67235
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NAME/KEY: UNSURE LOCATION: 1..111 OTHER INFORMATIO
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OTHER INFORMATION: Location
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                     TGAAGGAGGAAGCTTAAAGGTTAGCCTATAACCCCAAGAGTTAGCATCAAATGATATGAT
                                              TTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGCTGTCAGTGGCTCATAACG
  ACACCTAATCTAGTCAAGTAGATGCAATTCTTGTGAATATTGTATCTAGTTCTGGTCCCCT
              TGAAGGAGGAAGCTTAAAGGTTAGCCTATAACCCCAAGAGTTAGCATCAAATGATATGAT
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CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 28855
LENGTH: 1129
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 2750-709P
FILE REFERENCE: 2750-709P
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Pred. No. 1.1e-272;
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RESULT 4

US-09-708-427-27137

US-09-708-427-27137;

SEQUENCE 27137, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

FITLE OF INVENTION: SEQUENCE-DETERMINED DNF

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243p

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 27137

LENGTH: 942
                                                                                                                                                             ORGANISM: Arabidopsis thaliana FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..942
OTHER INFORMATION: any n = a, g,
NAME/KEY: misc_feature
LOCATION: 1..942
OTHER INFORMATION: Ceres Seq. ID
US-09-708-427-27137
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ACCGTACAAGCTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCAAT
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Pred. No. 3.6e-224;
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                                         APPLICANT: JOShua Z. Levin
APPLICANT: Ken Phillips
APPLICANT: Greg Budziszewski
APPLICANT: Fred Meins
APPLICANT: Fred Meins
APPLICANT: Zhenya Glazov
TITLE OF INVENTION: Methods of Controlling Ge
FILE REFERENCE: PB/5-31481A
CURRENT APPLICATION NUMBER: US/09/896,186B
CURRENT FILING DATE: 2002-04-04
NUMBER OF SEO ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 1
LENGTH: 942
                                                                                                                                                                                                 RESULT 5
US-09-896-186B-1
; Sequence 1, Application US/09896186B
; GENERAL INFORMATION:
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            09-896-186B-1
               TYPE: DNA
ORGANISM: Arabidopsis thaliana
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RESULT 6
US-09-620-393B-6112
US-09-620-393B-6112; Sequence 6112, Application US/09620393B; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED;
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1068P
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                                                                                           AAAAACCATCTTCTCACACTCAACGACCTTGAAGCAAAAATCTCACA
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96.1%;
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Pred. No. 3.6e-224;
0; Mismatches 35;
                    DNA
                    FRAGMENTS
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NAME/KEY: misc_feature

LOCATION: 1..507

OTHER INFORMATION: any n

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..507

OTHER INFORMATION: Ceres

US-09-620-393B-6112
                                                                                         RESULT 7
US-09-534-859-579/c
Occupance 579, Application
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       APPLICANT: Bush, David F.
APPLICANT: Last, Robert L.
APPLICANT: Levin, Irena M.
APPLICANT: Norris, Susan R.
APPLICANT: Parnell, Laurence D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: PLANT P
TITLE REFERENCE: 38-10(15493)
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Best Local S
Matches 491
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6112
LENGTH: 507
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ORGANISM: Arabidopsis
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APPLICATION
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PLANT POLYMORPHIC MARKERS 38-10(15493)B NUMBER: US/09/534,859
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Pred. No. 2.
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CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1127
SEQ ID NO 579
LENGTH: 118718
TYPE: DATE: CORGANISM: Arabidopsis thaliana
US-09-534-859-579
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US-09-803-736-579/c
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Best Local
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LENGTH: 118718
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Best Local Similarity
Matches 307; Conserv
                                                                                                                                 Matches 307;
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APPLICANT: Wilegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
FILE REFERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bush, David F. APPLICANT: Levin, Irena APPLICANT: Norris, Susan
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                 Local Similarity
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                                                                     TCGTTCCATCACCTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCCGTTGCCGAGCTAG
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             CGACGACGCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAA 96479
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Norris, Susan R.
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97.5%;
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Pred. No. 3.5e-73;
0; Mismatches 8
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US-09-906-226-15
Sequence 15, Application US/09906226
GENERAL INFORMATION:
APPLICANT: Butler, Karla
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
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Best Local Similarity 66.6%;
Matches 395; Conservative
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SEQ ID NO 15
LENGTH: 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                   GTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATC
                                                                                                                                                              ATTCATTCTGGAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAG
                                                                                                                                                                              TTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAG
                                                                                                                                                                                                                         GGAAAGGTAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTTCTACATCTA 468
                                                                                                                                                                                                                                        GGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATT
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               GGCCTTGCCTCACTAACTGAGACACTTGTTTTGCAAAGAGCTCCTGAAGCCAAACAGAATC
                                         AAAGGTGTGACGGATCTTTCTTTTCATGCTAATCAAAAGCTTGGTGGAGATCATAAGTGG
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; LENGTH: 1170
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; ORGANISM: Glycine
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SEQ ID NO 15
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APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant RNaseD-Like Genes
FILE REFERENCE: BB1467 US PRV
CURRENT APPLICATION NUMBER: US/60/218,993
CURRENT FILING DATE: 2000-07-17
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APPLICANT: Cahoon, Rebect
APPLICANT: Rafalski, Anto
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                 GATGCTTATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC
                                                        AGGCTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACG
                                                                                                              GTCTTGCATCTTTGACTGAAAAACTTCTATCAAAACAGCTTAAAAAGCCCCAACAAAATA
                                                                                                                                 GGCCTTGCCTCACTAACTGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCCAAACAGAATC
                                                                                                                                                                                       AAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGG
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  GATGCTTTTGCTTCTTGGTGTCTTTATCAGGCGATTAAAGATCTCCCGGACGC
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Pred. No. 8.2e-67;
0; Mismatches 198;
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US-09-849-529A-2068
; Sequence 2068, Application US/09849529A
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules Ar
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51893)B
; CURRENT APPLICATION NUMBER: US/09/849,529A
; CURRENT FILING DATE: 2001-05-07
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GENERAL INFORMATION:
APPLICANT: Havukkalla, Ilkka
APPLICANT: Shenk, Michael A.
TITLE OF INVENTION: Polynucleotides, Mat
TITLE OF INVENTION: Them, and Methods fc
FILE REFERENCE: 11000 1041U1
CURRENT APPLICATION NUMBER: US/09/605,698
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 25120
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US-09-605-698-9441
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US-09-605-698-9441
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Pred. No. 5.4e-40;
0; Mismatches 198
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Gaps

9;

Gaps

267

206

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; NUMBER OF SEQ ID NOS:
; SEQ ID NO 2068
; LENGTH: 584
; TYPE: DNA
; ORGANISM: GOSSYPIUM h:
; OTHER INFORMATION: Cld
US-60-196-868-2068
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ORANISM: Gossypium hirsutum
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(584)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3543-036-Q1-K1-F5
US-09-849-529A-2068
                                                                                                                                                                                                                                                             RESULT 13
US-60-196-868-2068
; Sequence 2068, Application US/60196868
; GENERAL INFORMATION:
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                                                                                                                          TITLE OF INVENTION: NUCLEIC ACTUAL TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21(51893)A
CURRENT APPLICATION NUMBER: US/60/196,868
CURRENT FILING DATE: 2000-05-09
CURRENT FILING DATE: 2000-05-09
CURRENT FILING DATE: 2000-05-09
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Matches
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PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 24076
SEQ ID NO 2068
LENGTH: 584
   Query Match
Best Local Similarity
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rter, David W.
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Clone ID:
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No.
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ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1434
OTHER INFORMATION: any n = a, g,
NAME/KEY: misc_feature
LOCATION: 1..1434
COTHER INFORMATION: Ceres Seq. II
US-09-708-427-65909
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-708-427-65909

Sequence 65909, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA

TITLE OF INVENTION: THEREBY
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 65909
LENGTH: 1434
                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                       376 CAACAAATATCATTCAGCGGTAAGATAGTTTACTGCAGGACACCTACAGAGGCGGAGAAA 435
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                                                        CGAGCAATGCAGCTTATTAAAGTTCTTGATACCAAGAGAGATGAATCTGGAATAGCTTTT
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   GTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCCGGGGAAGGTT
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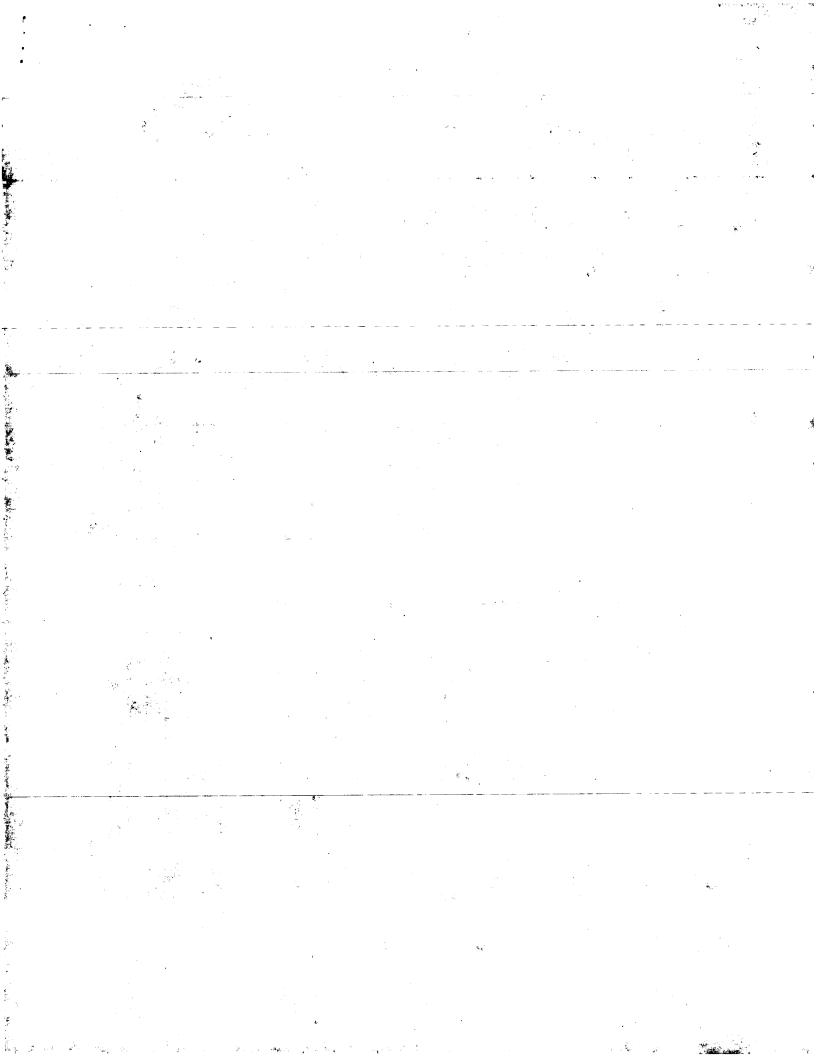
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LENGTH: 1434
TYPE: DNA
ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 83271, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                           FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..1434
OTHER INFORMATION: any n = a, g, c, t, ur
NAME/KEY: misc_feature
LOCATION: 1..1434
OTHER INFORMATION: Ceres Seq. ID 1962403
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Search completed: June 14, 2003, 09:12:07 Job time: 2843 secs



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Result
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Perfect score:
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1: /cgn2_6/ptodata/2/pna/U

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3: /cgn2_6/ptodata/2/pna/U

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7: /cgn2_6/ptodata/2/pna/U

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Match
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/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-531-113-705

US-09-531-113-705

US-09-724-676A-0395

US-09-724-676A-40395

US-09-896-186C-17

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Sequence 29, Appl	Sequence 7449, Ap	Sequence 220, App	Sequence 3, Appli	Sequence 7740, Ap	Sequence 2617, Ap	Sequence 3306, Ap	Sequence 171, App	Sequence 52767, A	Sequence 22, Appl	Sequence 21355, A	Sequence 21239, A	Sequence 284, App	Sequence 560, App	Sequence 104, App	Sequence 3109, Ap	Sequence 207, App	Sequence 76746, A	Sequence 35, Appl	Sequence 29, Appl	Sequence 53366, A	Sequence 53366, A	Sequence 86495, A

ALIGNMENTS

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APPLICANT: Fred Meins
APPLICANT: Enenya Glazov
TITLE OF INVENTION: Methods of Controlling Gerente Title Reference: 31481USNP
CURRENT APPLICATION NUMBER: US/09/896,186C
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/222,202
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
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US-09-896-186C-23
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SEQ ID NO 23
LENGTH: 1049
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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APPLICANT: JOSHUA Z. Levin
APPLICANT: Ken Phillips
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Best Local Similarity
Matches 1049; Conserv
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                                         CCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCAATAATATCCGTCGCCAATTGC
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RESULT 2
US-09-896-186C-1
Sequence 1, Application US/09896186C
GENERAL INFORMATION:
APPLICANT: JOSHUA Z. Levin
APPLICANT: Grey Budziszewski
APPLICANT: Grey Budziszewski
APPLICANT: Fred Meins
APPLICANT: Pred Meins
APPLICANT: Shenya Glazov
TITLE OF INVENTION: Methods of Controlling Ge.
FILE REFERENCE: 31481USNP
CURRENT APPLICATION NUMBER: US/09/896,186C
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/222,202
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
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RESULT 3
US-10-424-599-84537
Garuence 84537, Application
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; TYPE: DNA
; ORGANISM: Arabidopsis
US-09-896-186C-1
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Best Local Similarity
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Pred. No. 2.2e
0; Mismatches
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.2e-219;
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecul
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 84537
LENGTH: 1253
                                                                                                                              RESULT 4
US-10-389-048-9441
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Best Local S
Matches 395
                                                                                           Sequence 9441, Application US/10389048 GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
APPLICANT: Shenk, Michael A.
TITLE OF INVENTION: Polynucleotides, Materials Incorporating
TITLE OF INVENTION: Them, and Methods for Using Them
FILE REFERENCE: 11000.104101c1
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ORGANISM: Glycine max
FEATURE:
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les 395; Conserv
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Pred. No. 8.9e-66;
0; Mismatches 198;
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CURRENT APPLICATION NUMBER: US/10/389,04
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 25129
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 9441
LENGTH: 672
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-10-389-048-9441
                                                                                                                         Sequence 12947, Application US/09531113
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecularities of INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,11:
CURRENT FILING DATE: 2000-03-22
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; FEATURE:
; OTHER INFORMATION: Clone ID:
US-09-531-113-12947
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SEQ ID NO 12947
LENGTH: 579
TYPE: DNA
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                                              ORGANISM: Glycine
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                                                                                                                                             US/09/531,113
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                jC-gmf102220143d02a1
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Pred. No. 1.4e-39;
0; Mismatches 198
                                                                                                                                                                                             Molecules
                                                                                                                                                                                           And Other Molecules Associated With
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Query Match

13.6%;

Score 142.4;

DВ

5

Length 579

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With

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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: jC-gmfl02220143d02a1
US-09-531-113-12947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules An
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION UMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 48629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-531-113-12947
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SEQ ID NO 12947
LENGTH: 579
TYPE: DNA
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                                                                                                                                   GGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATT 539
                                                                                                                                                                                      CAAACTGCAATTGGATTTGACATTGAGTGGAAACCCACCTTCA-AAAAGGTGTTCCTCCC
                                                                                                                                                                                                           ATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCG
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   GTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTAT
                                                                         TTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAG
                                                                                                              GGAAAGGTAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTTCTACATCTA
                                                                                                                                                                                                                                                               GTAGAGAAAGCTGCAACAAAGCTCTTACAAATTCTCCAAGAAAAAAGGACCGACATGATG
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Pred. No. 7.5e-29;
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cches 121;
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                                                                         ; ORGANISM: Glycine m; OTHER INFORMATION: US-09-531-113-705
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US-09-531-113-705
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US-09-531-113-705
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Best Local S
Matches 172
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                                                                                                                              NUMBER OF SEQ ID NOS:
SEQ ID NO 705
LENGTH: 278
TYPE: DNA
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SEQ ID NO 705
LENGTH: 278
TYPE: DNA
Best Local Similarity Matches 172; Conserv
                                    Query Match
                                                                                                                                                                                    APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 48629
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APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic acid Molecules.
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
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mes 172; Conserv
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68.5%;
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                                                                                             ID: 700909421H1
Score 124.6;
Pred. No. 5e-7
0; Mismatches
 0;
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Pred. No. 5e-24;
0; Mismatches 79;
                   5e-24;
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                                    DB 6;
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APPLICANT: Byrum, Joseph R.
APPLICANT: Coombs, Brian E.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15444)C
CURRENT APPLICATION NUMBER: US/09/615,606A
CURRENT FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 91663
SEQ ID NO 75994
LENGTH: 278
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US-09-615-606A-75994
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                          CTCCCGGACGC
                                                         CTTCCTGATGC 892
                                                                                        CTAGAGTATGCTGCAACAGATGCTTTTGCTTCTTGGTGTCTTTATCAGGCGATTAAAGAT
                                                                                                                                                        AAAAAGCCCAACAAAATAAGACTGGGAAATTGGGAGGCTCCTGTTTTGTCAAAGGAGCAA 183
                                                                                                                                                                                                                          GGTGGAGATCATAAGTGGGGTCTTGCATCTTTGACTGAAAAACTTCTATCAAAACAGCTT 123
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Pred. No. 5e-24;
0; Mismatches 79;
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ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTMARE: Patentin version 3.2
SEQ ID NO 40395
LENGTH: 3255
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-40395
Sequence 40395, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 40395
LENGTH: 3255
TYPE: DNA
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US-09-724-676A-40395
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US-09-724-676-40395
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Best Local
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Similarity 54.1%;
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729 692 669 632 609

789 752

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APPLICANT: JOSHUA Z. Levin
APPLICANT: Ken Phillips
APPLICANT: Greg Budziszewski
APPLICANT: Greg Budziszewski
APPLICANT: Fred Melns
APPLICANT: Thenya Glazov
TITLE OF INVENTION: Methods of Controlling General APPLICATION NUMBER: US/09/896,186C
CURRENT APPLICATION NUMBER: 60/222,202
PRIOR APPLICATION NUMBER: 60/222,202
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US-09-896-186C-17
Sequence 17, Application US/09896186C
GENERAL INFORMATION:
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                                                         Query Match
Best Local Sim
Matches 272;
                                                                                                                                                                                                      PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 17
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Best Local
                                                                                                                                              LENGTH: 4299
TYPE: DNA
ORGANISM: Homo sapiens
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Similarity 54.1%;
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                                                      Score 111; DB 5; 1
Pred. No. 7.2e-20;
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Pred. No. 6.5e-20;
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US-09-949-001-3
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Sequence 3, Application US/09949001

Sequence 3, Application US/09949001

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO739

CURRENT APPLICATION NUMBER: US/09/949,001

CURRENT APPLICATION NUMBER: 60/231,323

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: 60/231,323

PRIOR FILING DATE: 2003-09-08

NUMBER OF SEQ ID NOS: 848

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 5208

TYPE: DNA
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
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 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTAGTTGGAATTGATGGTGACTCTGTGAAG
                                                                                                                               TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTTTTCTGAG
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                                                                                         AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT
                                                                                                                                                                AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT
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                                                        AGCAAATGTTACTTGTTCCACGTTTCTTCCATGTCAGTTTTTCCCCCAGGGATTAAAAATG
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Pred. No. 7.6e-20;
0; Mismatches 225
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678 872 752 498 438 632 378 572 318

609 572

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AGAGATGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA 45	Query Match 10.6%; Score 111; DB 8; Length 5208; Best Local Similarity 54.1%; Pred. No. 7.6e-20; Matches 272; Conservative 0; Mismatches 225; Indels 6; Gaps 2;	TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 70: US-10-374-077-70	SEQUENCE CHARACTERISTICS: LENGTH: 5208 base pairs	ORMATION 622-490 82-6031	ATTOREY,AGENT INFORMATION: NAME: ROSenman, Stephen REGISTRATION NUMBER: 43,058 REGISTRATION NUMBER: 100107.401D1	APPELICATION NUMBER: US/10/374,077 FILING DATE: 25-Feb-2003	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIAL Release #1.0, Version #1.30		ottle astington	CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRES	TITLE OF INVENTION: ANTIBODIES AGAINST GENE PRODUCTS RELATED TO WERNER'S SYNDROME NUMBER OF SEQUENCES: 209	Mulligan, John T. Schellenberg, Gerald D.	GENERAL INFORMATION: APPLICANT: Fu, Ying-Hui Yu, Chang-En	RESULT 14 US-10-374-077-70 ; Sequence 70, Application US/10374077	Qy 873 CTTAAGGACCTTCCTGATGCTGT 895	QY 813 AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872	QY 753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGĠAGTTTTATCCTCTGTCA 812	Qy 693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752	QY 633 CTTTFCCATGACTATGGAGTTAGTCAAAGATGTTGAGGATCTTTCAGATTTTAGCCAAC 692	610 TTGCTTGAAAATAAAGCAGTTAAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA
573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG	QY 516 AATTATTGTGATATTTTTTCATTCTGGTATCCCTCAAGTCTCCAACAT 572	Db 434 GATATTAGCATGAGTCTATCAGATGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 493 Oy 456 AGTTTAGAAAAGGTGTTCTCCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515	396 GATACCAAGAGAGAGTGAATCTGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCA	Query Match 10.6%; Score 111; DB 6; Length 5365; Best Local Similarity 54.1%; Pred. No. 7.7e-20; Matches 272; Conservative 0; Mismatches 225; Indels 6; Gaps 2;	; LENOTH: 5365 ; TYPE: DNA ; ORGANISM: Human US-09-949-001-9	NORE	NT FILING DATE: APPLICATION NUM FILING DATE: 20	; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF ; FILE REFERENCE: CL000789 ; CURRENT APPLICATION NUMBER: US/09/949,001	; sequence y, Application US/VYY4YULL ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al.	RESULT 15 US-09-949-001-9 15-09-949-001-9	Db 910 TTAGAGATTTTGGATGATACTGT 932	QY 873 CTTAAGGACCTTCCTGATGCTGT 895	OY 813 AAGCAGCAGTTACAATACGCAGCAAGCGATGCTTATGCTTCATGGCATCTTTACAAGGTT 872	OY 753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812	QY 693 CAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752	QY 633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTCAGATTTAGCCAAC 692	QY 573 CITATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG 632	Qy 516 AATTATTGTGATGTTATGCATATTTTCATTCTGGTATCCCTCAAAGTCTCCAACAT 572	QY 456 AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT 515	Db 433 GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA 492

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	911 TTAGAGATTTTGGATGATACTGT 933	911	рь
	873 CTTAAGGACCTTCCTGATGCTGT 895	873 (Qy
TEGETTTATTATTTACCGAAAT	851 GAGGACCAGAAACTGTATGCAGCCACTGATGCTTATGCTGGTTTTATTATTTACCGAAAT 910	851 (Db
CTTCATGGCATCTTTACAAGGTT 872	AAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGGCATCTTTACAAGGTT	813 /	Qy
ATTGGAGTAAATTTCCTCTCACT 850	AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT	791 /	В
ACTGGGAGTTTTATCCTCTGTCA	753 AAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA 812	753 /	Qy
ACCTGGAGCCTTAACAGTCTGGTTAAAACACCTCTTAGGT	SAAATGCACAGAG	731 /	Дb
CACTAACTGAGACACTTGTTTGC	CAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAACTGAGACACTTGTTTGC 752	693 (Qy
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AGGATCTTTCAGATTTAGCCAAC 692	633 CTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTTAGCCAAC	633 (Qy
SAATTGAAGGAGATCAGTGGAAA	611 TTGCTTGAAAATAAAGCAGTTAAAAAGGCAGGTGTAGGAATTGAAGGAGATCAGTGGAAA 670	611	Ф

Search completed: June 14, 2003, 09:27:35 Job time: 920 secs

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Minimum DB :
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5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

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ALIGNMENTS	AAY83171	ABP40469	ABB62792	ABB61252	AAU35540	AAR60653	AAG18363	AAG18364	AAM50929	AAY49564	AAW04254	ABG17672	AAB18185	AAG28362	AAG28363	AAR75647	AAG04684	ABB58154	AAM50932	ААМ50939	AAM50931	AAM50934	AAB93116	ABB55796	AAU39087	AAY29336	ABB11264	AAB80638	AAM50938	ABB91374	ABB62653	ABB71575	AAY14519	8	AAW59454
	Cell wall protein	Staphylococcus epi	Drosophila melanog	Drosophila melanog				Arabidopsis thalia	Arabidopsis RNase	Human lipoprotein	Human Factor V. H	Novel human diagno	-	Arabidopsis thalia		Thermophilic bacte	ຜ	Drosophila melanog			Arabidopsis RNase	ide 3'-5		polypepti	secreted	Human secreted pro	Human secreted pro	Environmental stre	Arabidopsis RNase	Herbicidally activ	Drosophila melanog	Drosophila melanog	Mouse WRN gene pro		Mouse WRN helicase

RESULT 1
AAG52858
ID AAG5
XX AAG5
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XX A 25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 29-MAR-1999 01-APR-1999 06-APR-1999 16-APR-1999 16-APR-1999 19-APR-1999 06-SEP-2000 EP1033405-A2 Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence. AAG52858 standard; Protein; 288 25-FEB-2000; Arabidopsis thaliana. Arabidopsis thaliana protein fragment SEQ ID NO: 67237. 18-OCT-2000 AAG52858; (first entry) 2000EP-0301439 990S-0121825.
990S-012548.
990S-0125788.
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pathway;
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 (SYGN ) SYNGENTA PARTICIPATIONS AG
                    01-AUG-2000; 2000US-222202P
                                       30-JUL-2001;
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                                                                              WO200210362-A2
                                                                                                Arabidopsis thaliana
                                                                                                                             RNase
                                                                                                                                               Arabidopsis RNase D related domain (3'-5'
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llarity 100.0%;
Conservative
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99US-0160981.
99US-0160981.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identified using different screening methods and search algorithms. The invention encompasses the suppression or increase of gene silencing in plants. This is achieved by altering the expression in the plant cell of a nucleotide sequence encoding a polypeptide, such as the present sequence, having an exonuclease domain, preferably a 3'-5' exonuclease domain, and especially an RNase D related domain. Expression of the nucleotide sequence is altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present is that of an Arabidopsis thaliana 3'-5' exonuclease domain, specifically an RNase D related domain. The 3'-5' exonuclease domain consists of 3 sequence motifs termed ExoI, Exand ExoIII. It was identified on the basis of homology to the Arabidopsis 3'-5' exonuclease sequence given in AAM50927. The nucleotide (see ABA91795-807) and polypeptide (see ABA927-39) sequences for 3'-5' exonuclease domains of the invention were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulating gene expression in plants for controlling gene silencing, comprises altering the transcription or translation of an endonuclease nucleotide sequence encoding a polypeptide comprising an exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL
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                                                                                                                                                                                                                                                                            NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120
                                                                               DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL
                                                                                                                                                                                                                                                                                                                                                                 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSAAPTVQATTSVHGHEEDPNQIPN
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                   LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSGS 288
                                                                                                                                                                                                                                                                                                                                             MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN
LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSGS
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AAG52857 standard; Protein; 298

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	18-OCT-2000 Arabidopsis t Protein ident hybridisation termination s
DOODER-0301439. 9805-0121485. 9805-0121485. 9805-0121486.	000 (first entry) sis thaliana protein fragment SEQ ID NO: 67236. identification; signal transduction pathway; metabolic pathway; ation assay; genetic mapping; gene expression control; promoter; ion sequence.
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9903 - 0141842 9903 - 014239 9903 - 014239 9903 - 014280 9903 - 014287 9903 - 0144085 9903 - 0144085 9903 - 014433 9903 - 014508 9903 - 014508 9903 - 0145145 9903 - 0145145 9903 - 0145145 9903 - 0145145 9903 - 0145218 9903 - 0145218 9903 - 0145218 9903 - 0145218 9903 - 0145315 9903 - 0145218 9903 - 0145218 9903 - 0145218 9903 - 0145313 9903 - 0145218 9903 - 0147204 9903 - 0147	S-014 S-013 S-014 S-014 S-014

27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;

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Similarity
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                                                                                                                                                              NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
                                   DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240
        LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSGS 288
                                                                                                                                                NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
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CC domain (Genrept accession CAB3681), specifically an RNase D related CC domain. The 3'-5' exonuclease domain consists of 3 sequence motifs CC domain. The 3'-5' exonuclease domain consists of 3 sequence motifs CC domains were identified using different screening methods and search CC algorithms. The invention encompasses the suppression or increase CC expression in the plant cell of a nucleotide sequence encoding a CC polypeptide, such as the present sequence, having an exonuclease CC expression in the plant cell of a nucleotide sequence encoding a CC polypeptide, such as the present sequence, having an exonuclease CC an RNase D related domain. Expression of the nucleotide sequence is altered by altering its transcription or translation. It is reduced e.g. by sense suppression, antisense suppression, homologous creduced e.g. by sense suppression, antisense suppression. CC recombination, the use of ribozymes, dominant-negative mutants, CC point or deletion mutagenesis, and increased by overexpression of the methods are useful for altering or stabilizing the expression of a nucleotide sequence of interest in a plant cell or plant. Suppressing or decreasing expression of the nucleic acid molecule cresults in decreased levels of post transcriptional gene silencing
                                                                                                                                                                                                                                                                                                                                                          Regulating gene expression in plants for controlling gene silencing, comprises altering the transcription or translation of an endonuclease nucleotide sequence encoding a polypeptide comprising an exonuclease
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gene silencing; t
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DB; ABA91795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phillips KL,
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/label- ExoII
260..270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= ExoIII
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08-OCT-1999 12-OCT-1999

15-SEP-1999 16-SEP-1999 20-SEP-1999 22-SEP-1999 23-SEP-1999 24-SEP-1999 28-SEP-1999 29-SEP-1999 04-OCT-1999 06-OCT-1999 07-OCT-1999

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Query Match Best Local Matches

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Best Local Sim
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05-MAR-1999

09-MAR-1999

23-MAR-1999

23-MAR-1999

24-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

23-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
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81; Conservative
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Pred. No. 2.1e-145;
1; Mismatches 4;
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il for identifying e activity.
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promoter;
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                                                                                                                                                                                Protein identification; signal transduction hybridisation assay; genetic mapping; gene etermination sequence.
                                                                                                           25-FEB-2000;
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                                                                                                                                                               Arabidopsis thaliana.
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Similarity 96.5%;
78; Conservative
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                                                                                                                                                                                                                                                                                                                                                        thaliana
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990S-0121825.
990S-0123548.
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Pred. No. 9.2e
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hes 8;
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expression control;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232
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                                                                                                                                                                                                                                              WRN gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 60.1%;
Similarity 96.6%;
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAVSDS
                                                                                                                                                                                                                                                                                   (first
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99US-0159330
99US-0159637
99US-0159637
99US-0159638
99US-0160741
99US-0160768
99US-0160770
99US-0160814
99US-0160981
99US-0160980
99US-0160980
99US-0161404
99US-0161404
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99US-0161361
99US-0161361
99US-0161392
99US-0161922
                                                                                                                                                                                                                                              product.
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99US-01
99US-01
99US-01
   96US-0632175
                                        96WO-US20785
                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                        phenotype
                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 896; DB 21;
Pred. No. 1.6e-87;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                           ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177;
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RESULT 10
AAM50935
ID AAM50935
AC AAM50
XX AM50
DT 15-MA
XX Enzym
KW Werne
XX Homo
XX 
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                                                                                                                                                                                              Enzyme;
Werner s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the human WRN gene product which is associated with Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype, as well as related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
   WO200210362-A2
                                                        Peptide
                                                                                             Peptide
                                                                                                                              Peptide
                                                                                                                                                                    Domain
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                    Human Werner syndrome protein
                                                                                                                                                                                                                                                                                                                                                         15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50935 standard; Protein; 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding the WRN useful for detection and treatment of Werner's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DARW-) DARWIN MOLECULAR CORP
(OSHI/) OSHIMA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-363671/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
: | : | | | | : : | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
75; Conserve
                                                                                                                                                                                                                                                              syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mulligan J,
                                                                                                                                                                                                                                                                                   3′-5′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX83001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAYAGEIIYRNLEILDDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAYASWHLYKVLKDLPDAV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLPFLEFTGSIVYSYDASDCSFLSE+----DISMSLSDGDVVGFDMEWPPLYNRGKL-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                              exonuclease; human; gene en
me protein; gene silencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2B; 153pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
                                                      /label= ExoI
135..150
/label= ExoII
209..219
                                                                                                                               /label= Exonuclease
78..87
                                                                                                                                                                      Location/Qualifiers
78..219
                                        /label= ExoIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       k; Score 352; DB
k; Pred. No. 7.6e
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
                                                                                                                                                                                                                                                                                                                    (3'-5' exonuclease domain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schellenberg GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Å
                                                                                                                                                                                                                                                              expression;
y; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
7.6e-28;
hes 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N gene product syndrome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ř
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1432;
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8,

Gaps

266

206 155

95

related

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RESULT 9
AAY14517
ID AAY1
XX AAY1
AC AAY1
XX JA-A
DT 31-A
XX Huma
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                              c of gene silencing in plants. This is achieved by altering the expression in the plant cell of a nucleotide sequence encoding a polypeptide, such as the present sequence, having an exonuclease domain, preferably a 3'-5' exonuclease domain, and especially an RNase D related domain. Expression of the nucleotide sequence is altered by altering its transcription or translation. It is reduced e.g. by sense suppression, antisense suppression, homologous reduced e.g. by sense roteins, double-stranded RNA, or insertional, point or deletion mutagenesis, and increased by overexpression of a nucleotide sequence of interest in a plant cell or plant. Suppressing or decreasing expression of the nucleic acid molecule results in decreased levels of post transcriptional gene silencing and improved expression of genes of interest. The 3'-5' exonuclease domain polypeptides are also useful for identifying compounds capable of altering 3'-5' exonuclease activity.
                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXOI, EXOII and EXOIII. Nucleotide (see ABA91795-807) and polypeptide (see ABM50927-39) sequences for 3'-5' exonuclease domains were identified using different screening methods and search algorithms. The invention encompasses the suppression or increase of gene silencing in plants. This is achieved by alternative transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present is that of human Werner syndrome protein (GenPept accession AAF06162), which includes an N-terminal 3'-5' exonuclease domain. The protein was identified in a homology screening with an Arabidopsis thaliana 3'-5' exonuclease domain (see AAM50927). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulating gene expression in plants for controlling gene silencing, comprises altering the transcription or translation of an endonuclease nucleotide sequence encoding a polypeptide comprising an exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN)
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 86-91; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-2000;
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DB; ABA91803.
216
                                267
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                                                                                                                                    96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exonuclease domains consists of 3 sequence motifs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) SYNGENTA
) NOVARTIS
                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                          Similarity 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNGENTA PARTICIPATIONS AG. NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
                                                                                  KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT
                                                                                                                                                  KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI
                              DAYASWHLYKVLKDLPDAV 285
                                                                                                                                KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL
                                                                                                                                                                                                   DLPFLEFTGSIVYSYDASDCSFLSE-----DISMSLSDGDVVGFDMEWPPLYNRGKL-G
                                                                                                                                                                                                                                     NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
DAYAGFIIYRNLEILDDTV
                                                              KNEVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT
                                                                                                                                                                                                                                                                                                                                            1432
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                                                                                       23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Budziszewski GJ,
                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                       Score 352; DB 23;
Pred. No. 7.6e-28;
41; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meins F,
                                                                                                                                                                                                                                                                                                         Length 1432;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glazov
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an
                                                                215
                                                                                              266
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RESULT 11

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AAW59454
ID AAW5
XX AAW5
AC AA
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AAW97841
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Best Local
                                                                mWRN
life
                                                                                                                           Murine mWRN polypeptide (WRN homologue).
                                                                                                                                                                           07-JUN-1999
                                                                                                                                                                                                                  AAW97841;
                                                                                                                                                                                                                                                              AAW97841 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a novel mouse WI associated with Werner's syndrome. The mother diagnosis of human Werner's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 18-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59454;
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                    Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV35114, AAV35115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Werner's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse WRN helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Werner's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mouse gene encoding protein - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EIJI-) EIJIN KENKYUSHO
                                                                span;
                                                                                  gene;
                                                                                                                                                                                                                                                                                                                                                                            207
                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATDAYASWHLYKVLKDLPDAV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKLESFYELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K----VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                                                            AATDAYAGLIIYQKIGNLGDTV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                             WRN gene; ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                              Protein; 1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WRN; helicase; murine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                         entry)
                                                                                  homologue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 339;
Pred. No. 1
                                                                                    Werner's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRN helicase protein which mouse WRN gene is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
L.8e-26;
les 72;
                                                                                  syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1401;
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RESULT 13
AAY14519
ID AAY14
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AC AAY14
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DT 31-AU
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                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of a polypeptide encoded by mWRN case AAX24302), the murine homologue of the human WRN gene associated with Werner's syndrome. A claimed assay for identifying a compound which extends life span comprises administering a compound to be tested to a mammal with a suppressed level of mWRN, and identifying slowing of at least one of the normal phenotypes of ageing in the mammal. A compound identified by this method inhibits the replication and/or accumulation of rDNA circles in a cell. The assay can be performed using a mWRN knockout mouse (also claimed). The mucleic acids can be used to produce mWRN polypeptides and as diagnostic probes and primers. mWRN polypeptides can be used to raise antibodies (for inhibiting activity of mWRN or for determining it is in tissues). The assay is based on the observation that in yeast cells, accumulation of ribosomal circular DNA is responsible for age-related enlargement and fragmentation of the nucleolus. A mutation in the yeast WRN homologue SGS1 causes premature ageing, suggesting a common ageing mechanism in all eukaryotes. Insight into the ageing process in model systems can provide insight into
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Mouse
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                         31-AUG-1999
                                                AAY14519
                                                                      AAY14519 standard; Protein; 1401
                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying agents that inhibit replication and accumulation of DNA circles - as potential agents for increasing the life span of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MASI ) MASSACHUSETTS INST TECHNOLOGY.
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DB; AAX24302.
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 WRN
                                                                                                                                                         264
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                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                           K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
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                                                                                                                                   AATDAYAGLIIYQKLGNLGDTV
                                                                                                                                                         AATDAYASWHLYKVLKDLPDAV
                                                                                                                                                                               VKLESEVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                        VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                               KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                                                                                              NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                              NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 69-72; 78pp;
                                                                                                                                                                                                                                                                                                                                                                             1401 AA;
                                                                                                                                                                                                                                                                                                                            Conservative
                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
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Pred. No. 1.8e-26;
2; Mismatches 72;
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RESULT 14
ABB71575
ID ABB71
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AC ABB71
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DT 26-MA
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DE Drosc
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KW Drosc
KW Pharm
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Best Local :
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29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the mouse WRN gene product. The corresponding human gene product (AAY14517) is associated with Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype,
              Drosophila;
                                              Drosophila melanogaster polypeptide SEQ ID NO 41517.
                                                                               26-MAR-2002
                                                                                                                                              ABB71575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding the WRN gene product useful for detection and treatment of Werner's syndrome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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(OSHI/) OSHIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                well as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mulligan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX83004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                              standard;
                                                                                                                                                                                                                                                         AATDAYASWHLYKVLKDLPD 283
                                                                                                                                                                                                                                                                                                                                                                            K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                         AATDAYAGLIIYQKLGNLGD 226
                                                                                                                                                                                                                                                                                          VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                          VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                                                                                                                                         KRSRVAVIQLCVSESKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                                                                                                                                                                                                                                       NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 6; 153pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1401 AA;
              developmental biology; cell signalling; insecticide
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                                                                              (first entry)
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95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
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                                                                                                                                              Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.1%;
36.0%;
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Pred. No. 1.7e-25;
3; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; autosomal;
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RESULT 15
ABB62653
ID ABB62
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AC ABB62
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invenueseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
Drosophila melanogaster polypeptide SEQ ID NO 14751.
                           26-MAR-2002
                                                      ABB62653;
                                                                               ABB62653 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                         41 TVQATTSVHGHEEDPNQIPNNIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILY
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                 YRELE 305
                                                                                                                                                                                                                                                                                                                                   SKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNY
                                                                                                                                                                          YKVLK 279
                                                                                                                                                                                                  WCNEVCETGGRWSLERLTNF IAKKAMDKSKKVRMSKWHVIPLDENQLMYAAIDVYIGQVI
                                                                                                                                                                                                                           LANOKIGGDKKWGLASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHL
                                                                                                                                                                                                                                                      CYIYQLTNVKKLPAALVALINHPKVRLHGVNIKNDFRKLARDFPEVTAEPLIEKCVDLGL
                                                                                                                                                                                                                                                                               CDVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDY-----GVSIKDVEDLSD
                                                                                                                                                                                                                                                                                                          FTESQDIAASADDVLQWVEKQKDE--VVPMAFDMEWPFSFQTG--PGKSAVIQICVDEKC
                                                                                                                                                                                                                                                                                                                                                               TPDVTEKLAMEEENP----PKRRSSRLTRSTRSMAEDGSPSPEKEKPEKLPFIKYKGAIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2000US-0614150
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                         (first entry)
                                                                               Protein;
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Best Local
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                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signaliling cell-rell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 14751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic a
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology;
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DL 281
                                                                                                                     DVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI
                                                 AGHKPEGLGKLSKTHLNYTLDKHWRLACSNWEAKTLEPKQLDYAANDALMAVAIYQKLCR
                                                                                                ALFRICHMKQIPQDLRELLEDDSVIKVGVAPQEDAMKLSHDYGVGVASTLDLRFLC--VM
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                                                                        GGDKKWGLASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLY-KVLK
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No. 1.7e-13;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 10:21:45 ; Search time 19 Seconds (without alignments) 1457.195 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-896-186B-24 1491 1 MSSSNWIDDAFTEEELLAID.....YASWHLYKVLKDLPDAVSGS 288

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26 27 28 29	2222	17 18 19 20 21	15 13 15 15 15 15 15 15 15 15 15 15 15 15 15	110 110 110	54321	Result No.
88 88 88 7 . 7	91 99.5	93.0 93 93 91.5 91.5	94.95 3.55	158 136.5 127.5 112.5 101 97.5	1439.5 339.5 339 339 330 179.5	Score
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1324 269 317 317	503 472 930	1020 2224 3079 237 758 473	4589 4589 416	123 910 239 217 876 445	313 1436 1401 1401 1401 582	Length I
8888	0000	222211	12212	0000000	88888	DB
T01508 I50504 A97511 AH2729	S13912 T47436 E64098	KFHU5 KFHU5 RGBYI2 H84732 H84732 T39210 S36553	F97039 A36121 T14914 C71620	E84752 S40930 A84777 T02548 T19246 E72674	T05256 T14895 T30247 T17452 H96604	ID
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tch repair e protein - z hetical prot inase [impor	aromatase (EC 1.14 protein kinase-lik	genome polyprotein coagulation factor probable GTPase-ac hypothetical prote 3-isopropylmalate L2 protein - human hypothetical protein - human	hypothetical prote aromatase (EC 1.14 dynein beta heavy protein with Eg1-1	hypothetical prote	hypothetical prote DNA helicase 1 - A Werner syndrome pr Werner syndrome pr probable 3'-5' exo	Description

RESULT 2
114895
DNA helicase 1 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14895
R:Yan, H:; Chen, C:Y:; Kobayashi, R.; Newport, J.
Nature Genet. 19, 375-378, 1998

2 C88558 2 T03558 2 T93558 2 E96753 2 T40342 2 E88492 2 E88492 2 E72450 2 T44362 2 I40371 1 A37797 1 BYECPR 2 T10193 2 T10193 2 T10193

ALIGNMENTS

181 181 181 241 241	QY 1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSAAPTVQATTSVHGHEEDPNQIPN	A;Accession: T05256 A;Molecule type: DNA A;Residues: 1-313 <bev> A;Cross-references: EMBL:AL035528 A;Cross-references: EMBL:AL035528 A;Experimental source: cultivar Columbia; BAC clone F18A5 C;Genetics: C;Genetics: A;Map position: 4 A;Introns: 86/1; 143/1; 186/3; 239/3 A;Introns: 86/1; 143/1; 186/3; 239/3 A;Note: F18A5.260 Query Match Sest Local Similarity 95.3%; Pred. No. 5.6e-117; Best Local Similarity 95.3%; Pred. No. 5.6e-117; Matches 281; Conservative 1; Mismatches 4; Indels 9; Gaps</bev>	RESULT 1 T05256 T05256 Typothetical protein F18A5.260 - Arabidopsis thaliana (protein S2-Apr.1999 #text_change 23-Jul-1999 C; Date: 23-Apr.1999 #text_change 23-Jul-1999 C; Accession: T05256 R; Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, February 1999 A; Reference number: 215405
		iaps 1;	1999 Mewes, H.W.; M

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RESULT 3
T30247
T30247
Werner syndrome protein typeI - mouse
N; Alternate names: Wrn typeI protein
C; Species: Mus musculus (house mouse)
C; Date: 22-Oct-1999 #sequence_revision
C; Accession: T3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Imamura, O.; Ichikawa, K.; Yamabe, Y.; Goto, M.; Sugawar Genomics 41, 298-300, 1997
A;Title: Cloning of a mouse homologue of the human Werner A;Reference number: Z20785; MUID:97288537; PMID:9143515
A;Accession: T30247
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A; Residues: 1-1401 < IMA>
A; Cross-references: EMBL: D86526; NID: g2130972; PIDN: BAA20269.1;
Cross-imantal source: strain BALB/c; testis/spleen
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A; Residues: 1-1401 <I
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)2; Conservative
                                                                                                                                                    K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG 203
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                           AATDAYASWHLYKVLKDLPDAV
                                                             VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                               VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                  KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                       NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                     NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
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36.6%;
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35.0%;
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                                                                                                                                                                                                                                                                      Score 339; DB 2; red. No. 9.1e-21; Pred. No. 9.1e-21; 72;
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                        Length 1401;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, F. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ky; M.; D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ky; M.; D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ky; M.; Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: H96604
R;Theologis, A.; Ecker, J.R.; Palm,
Chin, C.W.; Chung, M.K.; Conn, L.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable 3'-5' exonuclease [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: Wrn protein
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T17452
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                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                       A; Gene: F14G9.8
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-582 <STO>
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A; Residues: 1-1401 <PAE>
                                                                                                                                                                                                                                                    A;Cross-references:
                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
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;Gene: Wrn
                                                                                                             Query Match
Best Local
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Best Local :
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  377
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                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 36.(
72; Conservative
                     GIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSN--YCDVMHIFHSG---IPQSLQHLIE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATDAYASWHLYKVLKDLPD
||||||| :|: | :| |
AATDAYAGLIIYQKLGNLGD
GCRVVGIDCEWKPNYIKGSKQNKVSIMQIGSDTKIFILDLIKLYNDASEILDNCLSHILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
                                                                                                                                                                                                                                                    GB:AE005173; NID:g11094727; PIDN:AAG29662.1;
                                                                                                             12.0%;
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                                                                                       Score 179.5; DB 2;
Pred. No. 1.8e-07;
6; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 330; DB 2; pred. No. 5.5e-20; Pred. No. 5.71;
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                                                                                          Indels
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; Dewar,
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A;Introns: 64/1; 336/2; 382/2; 447/2; 681/2; 810/1; 852/2 Query Match 9.2%; Score 136.5; DB 2; Length 910; Best Local Similarity 24.8%; Pred. No. 0.0017; Matches 77; Conservative 34; Mismatches 110; Indels 89; Gaps 13; Qy 12 TEEELLAIDAIEASYNFSRSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPRSIT 71 :	hetical protein ZK1098.8 cles: Caenorhabditis eleg e: 06-Jan-1995 #sequence_ ession: S40930 mas, K. tted to the EMBL Data Lib erence number: S40923 ession: S40930 tus: preliminary ecule type: DNA dlues: 1-910 <tho> ss references: EMBL: Z2217 etics:</tho>	Query Match 10.6%; Score 158; DB 2; Length 123; Best Local Similarity 79.5%; Pred. No. 1.6e-06; Matches 31; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Qy 190 GIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGL 228	hypothetical protein At2g34110 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E84752 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84752 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-123 <sto> A;Cross-references: GB:AE002093; NID:g2342731; PIDN:AAB67629.1; GSPDB:GN00139 C;Genetics: A;Map position: 2</sto>	Qy 181 DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI 220 221 GGDKKWGLASITETLVCKELLKPNRIRLGNWEFFYPLSKOQLQYAATDAYASWHLVKVLKD 280
RESULT 9 T02548 T02548 T02548 T02548 N;Alternate names: hypothetical protein T26B15.5 N;Alternate names: hypothetical protein T26B15.5 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02548; G84733 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykesubnitted to the EMBL Data Library, July 1998 A;Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence. A;Reference number: Z14678 A;Accession: T02548 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA	Qy 121 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFH-SGIPQSLQHLI 179	A;Gene: At2936110 B: Conservative 8.6%; Score 127.5; DB 2; Length 239; Best Local Similarity 25.1%; Pred. No. 0.0017; Best Local Similarity 25.1%	RESULT 8 A84777 A94777 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: A84777 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 400, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A84777 A;Status: preliminary A;Residues: 1-239 <sto> A;Cross:references: GB:AE002093; NID:94678223; PIDN:AAD26968.1; GSPDB:GN00139</sto>	Qy 120 TKRDESGIAFYGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHI 166

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hypothetical protein C14A4.4 - Caenorhabditis elega
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T19246
R;MCMNITTAY, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-217 <STO>
A; Cross references: GB: AEC02093;
C; Genetics:
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R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, i
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
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A; Map position: 2
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                                                                                                                                                                                                                                                                A:Map position: 2
A:Introns: 80/2; 557/2; 731/3; 833/1
                                                                                                                                                                                                                                                                                                                                     A;Cross-réferences: EMBL:Z49909; P
A;Experimental source: clone C14A4
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-876 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T19246
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A;Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298537
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Best Local :
                                                                                                                                                                                                                Local Similarity
                                                                                                                           183 QMVVLEKPQKTYNI----SSDNSQAPFSSKLTVKHHAIEKRTGIVLHDDDESG-----RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 QICVDSNYCDVMHIFH-SGIPQSLQHLIEDSTLVKVGI--GIDGDSVKLFHDYGVSIKDV
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                                                                                                                                                                                                  64:
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                      LDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICV-DSNY-CDVMHIF-HSGIPQS
                                                          DWISAETETEEEHPYIAEILHFKVPEAQLKSAECLKFTALKDTPLTMIDTKEKLEALTKT
                                                                                      QLPRSITSS-----TSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKV
                                                                                                                                                         ELLAIDAIEASYNFSRSSSSSSSSAAP-----TVQATTSVHGHEEDPNQIPNNIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHDVY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATDAY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHIRHYLHPLL-----LSSSFETIVKVYLGHEGVTKDKELCMSNWGARSLSHDQIVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLSDLANQKIGGDKKWGLASLTETLV-----CKELLKPNRIRLGNWEFYPLSKQQLQYA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLCVGTR-CLIIQLSHCKYVPDVLRSFLEDQTITFVGVWNSQDKDKLERFH-HQLDIWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGERLIVTVTHTPSVIRRWIHSIRFVSRLRLSHPLV-VGLGVQWTP--RGSDPPPDI--L
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21.1%;
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25.4%;
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                                                                                                                                                                                                                                                                                                                                                   PIDN:CAA90108.1;
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Pred. No. 0.03
38; Mismatches
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                                                                                                                                                                                                              Score 101;
Pred. No. 2;
                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                             Length 876
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E.; Umayam, L.; Tallon, L.
                                                                                                                                                                                             54;
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                                                                                                                                                                                             Gaps
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C;Accession: F97039
                                                                                                                           hypothetical protein CAC1132 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: F97039
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Pred. No. 1
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                                                                                                           K.S.;
                                                        Solvent-Producing Bacterium
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R;Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Ta awa, H; Takamiya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-445 <KAN>
A;Residues: 1-445 <KAN>
A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79797.1; PID:d1043583; PID:g
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_ch
                                                              NRIR-----LGNWEFYPLSKQQL-----QYAATDAYASWHLYKVLK
                                                                                                                                                                                              VKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI-GGDKKWGLASLTETLVCKELLKP
                                                                                                                                                                                                                                                                              DVDRLVRLVAEWARA-----NPASAKVFLDS------LSAELERL-----
                                                                                                                                                                                                                                                                                                                                         DI-----EWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIEDSTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                     VSRA-YFYQMRRGLR-----PISDSILERLLELATDDDLAGIPFFAPYVDYQRVKGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFV------GL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKNSTAAPSSSHAEGESTADVLGYEGVEVLPEPKDVPQEARRQLLNLLAERGKVKPSTLG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSSSAAPTV-----QATTSVHGHE-----EDPNQIPNNIRRQLPRSITSSTSYKREPLS
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                                                                                                                                       ----GLVGKAIK-----VSERHVREFEGYLEARVRSGDMDPGTAG-----
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YVLTKQALRGLIRRYQASQPGVADHIYKSLK
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Zeng, Q.;

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A;Gene: CYP19: human cytochrome P450 CYP19; cytochrome P450 homology C;Kuperfamily: human cytochrome P450 CYP19; cytochrome P450 homology C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; F;303-459/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-2,'FQ',5-9,'Q',11-87,'C',89-100,'L',102-122,'VVH',126,'HAR',130-187,'L',18492,'SPRNS' <LEP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:M33986; NID:g203804; PIDN:AAA41044.1; PID:g203805 R;Lephart, E.D.; Peterson, K.G.; Noble, J.F.; George, F.W.; McPhaul, M.J. Mol. Cell. Endocrinol. 70, 31-40, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A: Posidues: 1-508 <HIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matase cDNA and 5' genomic DNA.
A; Reference number: A36121; MUID:90220647; PMID:2157976
A; Accession: A36121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: A36121; S16901; S26817
R;Hickey, G.J.; Krasnow, J.S.; Beattie, W.G.; Richards, J.S.
Mol. Endocrinol. 4, 3-12, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aromatase (EC 1.14.14.-) cytochrome P450 19 N;Alternate names: cytochrome P450 arom
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A;Molecule type: DNA
A;Residues: 1-488 <KUR>
A;Residues: 1-488 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79105.1; PID:g15024051; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1132
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    210
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34; Conservative
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                                                                                                                                                                                                        RFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEW---RPSFRKGVL-PGK 148
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ESSIVKKIQGYFNAWQALLIKPNIFFKISWLYRKYERSVKDLKDEIEILVEKKRQKVSSA 269
                                             GDSVK---
                                                                                IRMVEVCVESIKQHLDRLGDVTDNSGYVDVVTL-----MRHIMLDTSNTLFLGIPLD
                                                                                                                              VATVQICVD--
                                                                                                                                                                 RFG-----SKRGLQCIGM-----HENGIIFNNNPSLWRTVRPFFMKALTGPGL
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                                                                                                                         SNYCDVMHIFHSGIPQSLQHLIED-STLVKVGIGID 192
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                                       LFHDYGVSIKDVED - - - - LSDLANQKIGGD
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                                                                                                                                                                         R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, Science 288, 116-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                        protein with Eg1-like 3'-5' exonucl. domain PFB0215c - malaria parasite (Plasmodium C;Speckes: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: C71620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 286/3; (C;Superfamily: dyna C;Keywords: P-loop
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A;Molecule type: DNA
A;Residues: 1-4589 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000 C;Accession: T14914
C;Accession: LiM; Gibson, T.M.; Asai, D.J.; Forney, J.D.
R;Lincoln, L.M.; Gibson, T.M.; Asai, D.J.; Forney, J.D.
submitted to the EMBL Data Library, June 1999
A;Description: A gene knockout reveals that dynein beta heavy chain is requested.
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T14914
                                       A; Experimental source: C; Genetics:
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A; Residues: 1-416 <GAR>
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A; Accession: T14914
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1 aplysia cal
2 mycoplasma
5 streptococc
2 drosophila
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Castro E., Ogburn C.E., Hunt K.E., Tilvis R., Louhija J.,
Penttinen R., Erkola R., Panduro A., Riestra R., Piussan C.,
Deeb S.S., Wang L., Edland S.D., Martin G.M., Oshima J.;
"Polymorphisms at the Werner locus: I. Newly identified polymorphisms of the Werner locus: I. Newly identified polymorphisms at the Werner locus: I. Newly identified polymorphisms of infinity in a population of Finnish centenatians:"

Am. J. Med. Genet. 82:399-403(1999).

-I- FUNCTION: ESSENTIAL FOR THE FORMATION OF DNA REPLICATION FOCATION FOR REPLICATION ESSENTIAL FOR THE FORMATION OF DNA REPLICATION ESSENTIAL FOR THE FORMATION OF DNA REPLICATION FOR 
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Meissitzer C., Ruppitsch W., Weirich-Schwaiger H., Weirich Jabkowsky J., Klein G., Schweiger M., Hirsch-Kauffmann M.;
"Werner syndrome: characterization of mutations in the WRN g affected family.";
                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vidal V., Bay J.-O., Champomier F., Grancho M., Beauville Glowaczower C., Lemery D., Ferrara M., Bignon Y.-J.;
"The 1396del A mutation and a missense mutation or a rare of the WRN gene detected in a French Werner family with a phenotype and a case of an unusual vulvar cancer.";
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                                                                                                                                                                                                           Genew;
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                                                                                                                         InterPro;
                                                                                                                                                InterPro;
                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                    L; L76937; AAC41981.1; -.

L; AF091214; AAC63361.1; -.

L; AF181897; AAF06162.1; -.

L; AF181896; AAF06162.1; -.

SW; HGC:12791; WRN.
                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration seen the Swiss institute of Bioinformatics and the EMBL outstation buropean Bioinformatics institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
    PF00270;
PF00271;
PF00570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Med.
); IPRO02562; 3_5_exc

); IPRO01410; DEAD.

); IPRO01131; HRDC.

); IPRO01650; Helicas

); IPRO04589; RecQ.

'00270; DEAD; 1.

'00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.
                                                                                                                                                                                                                                                                                                                              requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167244; PubMed-10069711; Ogburn C.E., Hunt K.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T., Nakura J., Oshima J., Kamino K., Higaki J., Edland S.D., Martin G.M., Genet. 70:103-103(1997).
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Best Local S
Matches 75
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009053; 009050; 992242;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Werner syndrome helicase homolog.
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                                 "Cloning of a mouse homolo assignment to 8A4 by fluor Genomics 41:298-300(1997).
                                                                                                       STRAIN-BALB/c; TISSUE-Testis, and MEDLINE-97288537; PubMed-9143515; Imamura O., Ichikawa K., Yamabe Y
                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                 WRN.
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Hydrolase; Helicase; ATP-binding;
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C -> R (ASSOCIATED WITH MYOCARDIAL INFARCTION).
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                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                           Goto M.,
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                                                  human Werner syndrome situ hybridization.";
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Matches 74
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Pfam; PF00570; HRDC; 1.
Pfam; PF01612; 3_5_exonuclease; 1
SMART; SM00474; 35EXOC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
-i- FUNCTION: MAY BE INVOLVED IN THE CONTROL (
-i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicase;
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"Nucleolar localization of the Werner syndrome protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fam;
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[nterPro;
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rPro; IPR002562; 3_5_exonuclease.
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een the Swiss Institute of Bioinformatics and the En
European Bioinformatics Institute. There are no resti
by non-profit institutions as long as its content
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                                         37
                                                                                                                                       Similarity
K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                       NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                          NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
                                                                                                                                                                                                                    535 542

535 635

1115 1194

1115 1197 1390

101 101

101 228 228

228 228

459 459

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468 619 619

800 1011

1145 1145

1145 1145

1181 1182

1308 1308

1356 1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR00614; recq;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAA20270.1; -. BAA20269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC78077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRDC;
                                                                                                                                                                                                   3
                                                                                                                                     22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RecQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicase_C
                                                                                                                                                                                                 157256 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear
                                                                                                                                                                                                           V -> K (IN N- A -> S (IN N- A -> T (IN REF. 3).
VG -> LE (IN REF. 3).
VG -> A (IN REF. 3).
                                                                                                                     42;
                                                                                                                                                                                                                POLY-SER.

N -> S (IN)

L -> S (IN)

L -> S (IN)

K -> T (IN)

C -> R (IN)

C -> R (IN)

C -> R (IN)

C -> C 
                                                                                                                                     Score 339;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Werner's gene and cloning of its
                                                                                                                                                                                               949060992467FB8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOX.
                                                                                                                                                                                                                                                                                                REF.
                                                                                                                                                                                                                                                                                                                                                                                               REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY. RECO SUBFAMILY
                                                                                                                                   DB 1;
.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guarente L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF GENOMIC
                                                                                                                                                        Length 1401;
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         he EMBL outstation restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STABILITY
                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration -
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse
                                     86
                                                                            147
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RESULTATION OF THE PROPERTY OF
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen J.
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y068_CAEEL STA
P34607;
01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 105.6 kDa protein ZK1098.8 in chromosome
                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 910 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01612; 3_5_exonucl
SMART; SM00474; 35EXOC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; ZK1098.8; CE00370. InterPro; IPR002562; 3_5_ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZK1098.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R., Watson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Z22176; CAA80137.1; -. S40930; S40930.
369 SKLREAKELLVRRKTLQVP---LNGEQLFVFENERRTQIHMVKTESEMN----YLCSEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264
                                                        72
                                                                                                                                             12 TEEELLAIDAIEASYNESRSSSSSSSSSSSSAPTVQATTSVHGHEEDPNQIPNNIRRQLPRSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                          Similarity
                                                        SSTSYKRFPLSRCRARNFPAMRFGGRILY-----SKTATEVDKRAMQLIKVLD
                                                                                                                TEKQ---IDAICFAIYLGIASSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATDAYAGLIIYQKLGNLGDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATDAYASWHLYKVLKDLPDAV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKLESFYELTDVANEKLKCAETWSLNGLYKHYLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO RIBONUCLEASE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                _5_exonuclease;
                                                                                                                                                                                                                                                       9.2%;
                                                                                                                                                                                                                                                                                                                                             105569 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3_5_exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weinstock L., Wilkinson-Sproat
                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                  Score 136.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                             5512D15423517FCD CRC64;
                                                                                                                                                                                                                                                          No. 0
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                                                                                                                                                                                                                             ).0011;
nes 110;
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                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditida;
                                                                                                                                                                                                                                                                                  Length 910;
                                                                                                                                                                                                                             Indels
                                                                                                                ---YQLP-NVMRDFFRQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     III
                                                                                                                                                                                                                             89;
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.,
  421
                                                                                                                                                                  71
                                                                                                                368
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RESULT 4
CPV1_RAT
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                             Matches
                                                     Query Match
                                                                              BINDING
SEQUENCE
                                                                                                                                                                                                                                               use by modified
                                                                                                                                                                                                                                                                         This SWI
between
the Euro
                                                                                                                               PRINTS; I
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hickey G.J., Krasnow J.S., Beattie W.G., Richards J.S.; "Aromatase cytochrome P450 in rat ovarian granulosa cells before after luteinization: adenosine 3',5'-monophosphate-dependent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 19 (Aromatase) (EC 1.14.14.1)
synthetase) (P-450AROM).
                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 ÷
                                                                                                                                                                                                                                                                                                                                                                                                      Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYP19 OR AROM
                                                                                                                                                                                                                                                                                                                                                                                                                  independent regulation. Cloning and sequencing
and 5' genomic DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90220647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lickey G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                         Local
                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content by
                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Membrane-bound.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: RH + reduced flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                      5' genomic DNA.";
Endocrinol. 4:3-12(
FUNCTION: CATALYZES
                                                                                                                                                                                                                                                                                                                                                   oxidized flavoprotein +
                                                                                                                                                                                                                                                                                                                                                                             C19 ANDROGENS.
                                                                                                                                                                                  A36121; A36121
                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                              M33986; AAA41044.1;
                             42;
                                       Similarity
REGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEW---RPSFRKGVL-PGK 148
                                                                                                                                 PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSDEPAPVYVGFDSEWKPSNLTAVHDSKIAIIQLFFKNCVWLVDCVELEKANMAD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAYASWHLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAENVCDIDMEILELPKKTFKLADLTHYLLGLELDKTE--QCSNWQCRPLRKKQIVYAAL
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                                                                                                                   transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHSGIPQSLQHLIEDSTLVKVGIGIDGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- DWWQKFASRLFGDSPVKVVGFDMRNDLDAMATIPALKSSMKI----
                                                                              437
508
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0647; PubMed=2157976;
Krasnow J.S., Beatti
                                                                              ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                           P450.
                                                                                                                                                                                                                                                                                                                                                                                                      4:3-12(1990)
                                                                             437 I
58411 MW;
                                                                                                                  Oxidoreductase;
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                                     6.4%;
                                                                                                                                                                     Cytochrome_P450
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                                     Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       FORMATION OF
                          Pred. No. 1.6
5; Mismatches
                                                                          HEME.
COADFB0FD80AB352 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                  Monooxygenase;
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                                   DB
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                          Indels
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                                                                                                                  Membrane;
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Murinae; Rat
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01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein (Contains: Capsid protein (protein (Envelope protein M); Major envelope
protein (Envelope NS2B; Protease/helicase (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P09732;
Q88788;
                                                                                                                                                                                                                                                                                                                                                                                       Trent D.W., Kinney R.M., Johnson B.J.B., Vori Deubel V., Rice C.M., Hahn C.; "Partial nucleotide sequence of St. Louis enstructural proteins, NS1, NS2A, and NS2B."; Virology 156:293-304(1987).
                                                                                                                                                                                                                                                          This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-87122172; PubMed-3027980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
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                                                                                                                                                                                                                                                                                        HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RAR REPLICATION.

CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the varieties polyprotein, commonly with asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1.

SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED E LIEOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN MAND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX (
                                                                                                                                                                                                                                                                                  PROTEIN M AND GLYCO PROTEIN C AND MRNA.
                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encephalitis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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and NS2B.";
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Q88784; Q88785; Q88786; Q88787;
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e (EC 3.4.2
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n E; Nonstructural
.21.98) (NS3)]
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InterPro; InterPro; Pfam; use by non-profit institutions as long modified and this statement is not removed. Pfam; EMBL; M16614; AAA47786.1; -. PIR; A27531; GNWVS5. the InterPro; InterPro; InterPro; InterPro; InterPro; entities requires a European Bioinformatics Institute. The by non-profit institutions as long PF00869; Flavi_glycoprot; PF00948; Flavi_NS1; 1. PF01002; Flavi_NS2B; 1. PF01003; Flavi_capsid; 1. an email to license@isb-sib.ch). IPR001157; IPR000752; IPR000487; IPR001122; IPR000336; IPR002535; ; Flavi_NS1.
; Flavi_NS2B.
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P1259; Q14285;
O1-CCT-1989 (Rel. 12, Created)
O1-FEB-1994 (Rel. 28, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
The sequence update of the seq
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  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pfam; PF01570; Flavi_propep; 1.
Pfam; PF02832; Flavi_glycop_C; 1.
ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1.
Polyprotein; Glycoprotein; Core protein; Coat protein;
Polyprotein; Hydrolase; Helicase; ATP-binding; Tr
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47; Conser
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Pred.
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CELLULAR AMINOPEPTIDASE.
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Craniata; Ve
Catarrhini;
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No. 9
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                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                         -GWKKWGKTLFVEP-
                                                                                                                                                                                                                                                                                                                                                               277
  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                      cofactor).
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Dirven R.J., de Ronde H., van der Velden P.

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MEDLINE-87260886; PubMed-3110773;
Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Jenny R.J., Kaufman R.J., Mann K.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-92232668; PubMed-1567832;

Cripe L.D., Moore K.D., Kane W.H.;

"Structure of the gene for human coagulation
Biochemistry 31:3777-3785(1992).
                                                                                                                                                                                                                                                                                                                                                                                        Pittman D.D.,
Kaufman R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shen N.L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE F
TISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1188-1215 AND 1315-2224 MEDLINE=86313665; PubMed=3092220;
                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9
                                                                                                                                                                                                                                                                                                 Hortin G.L.;
                                                                                                                                                                                                                                                                                                             MEDLINE=90366699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edgington T.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93203619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 26:6508-6514(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88107560; PubMed=2827731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-1600 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94264012; PubMed-8204629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                       "Sulfation of tyrosine residues in Blood 76:946-952(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.-T.,
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                                                                                                                                                                                                                                                                                                              PubMed=2168225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8454869;
S.-T., Pyati J.,
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                                                                                                                                                                                                                                             ANGSTROMS)
                                                                                                                                                                            membrane-binding C2
                                                                                                                                                                                                                                                                                                                                                                                                    Michnick D.,
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                                                                                                                                                                                                                   Quinn-Allen
                                                                          ., Rosendaal F.R.,
n P.A., Reitsma P.
associated with r
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Kong
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                                                                                                                                                                                                       Kane
                                                                            resistance
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A28b.

A3; 1C2S; 26-..

PDB; 1CZV; 26-NOV

PDB; 1CZV; 26-NOV

Genew; HGNC:3542; F.

MIM; 227400; -..

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williamson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vnain, noncovalently bound. The is calcium-dependent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR, factor Va (formation of a heavy chain at the N-
terminus and a light chain at the C-terminus).

PTM: SULFATION IS REQUIRED FOR EFFICIENT THROWSIN CLEAVAGE AND
ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.

DISEASE: OWNERN PARAHEMOPHILIA, AN HEMORRHAGIC DIASTESIS, IS DUE
TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN F5 RESULTS IN A
FORM OF THROMSOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR
MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST TH
A SLIGHT THROMSOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH
2 PLASTOCYANIN-LIKE REPEATS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \ensuremath{\text{PTM}}\xspace . Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES WITH FACTOR XA TO ACTIVATE PROTHROWSIN TO THROWSIN. SUBUNIT: FACTOR VA 1s composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPLANTATION.
                                                                                                                                                                                                                                  A25897; A25897
A28028; A28028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L32779;
L32755;
L32756;
L32757;
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                                                                                                                                                                                                                                                                                             M14335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                 26-NOV-99.
; 26-NOV-99.
; 26-NOV-99.
NC:3542; F5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00079; MULTICOPPER_OXIDASE1; PROSITE; PS01285; FA58C_1; 2. PROSITE; PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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MIM; 227310;
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58; Conserv
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H
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                                                                                                                                          YSHENLIEDFNSGLIGPLLICKK------GTLTEGGTQKTFDKQIVLLFAVFDESK-
                                                                                                                                                            RQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRD
                                                                                                                                                                             ASYLDHTFPAEKM--DDAVAPGREYTYEWSISEDSGPT
                                                                                                                                                                                              SNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIR
                                                                                                                        ESGIAFVGLDIEWRPSFR-----KGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHL
                                   GMQAYIDIKNCPKKTRNLKKITREQRRHMKRWEYFIAAEEVIWDYAPVIPANMDKKYRSQ
                                                                     SSGPEL--FSIHFNGQVLEQNHHKVSAITLVSATSTTANMTVGPEGKWIISSLTPKHLQA
                                                                                     IEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLT-----
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                                                                                                        SWSQSSSLMYTVNGYVNGTMPDITVCA-----
                                                                                                                                                                                                                       6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cu-oxidase
FA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease mutation;
                                                   ETLVCKELLKPNRIRLGNWEFYPLSKQQL-QYAAT-----DAYASW
                                                                                                                                                                                                                42;
                                                                                                                                                                                                               Score 93; DB
Pred. No. 17;
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        F5/8 TYPE A 1.
PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
F5/8 TYPE A 2.
                                                                                                                                                                                                                                                                                              2-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEAVY CHAIN.

ACTIVATION PEPTIDE (CONNECTING REGION)
                                                                                                                                                                                                                                                                                                                                                                         TO 14 AA REPEATS IN BOVINE FA5.
35 X 9 AA APPROXIMATE TANDEM REPEATS
[TNP]-L-S-P-D-L-S-Q-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASTOCYANIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COAGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                      ×
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                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                      TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTOR
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                                                                                                                                                                                                                124;
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                                                                                                                                                                             -----HDDPP--CLTHIY
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                                                                                      232
                                                                                                        260
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RESULT 7
IRA2_VEAST
ID 2_VEAST
ID
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C P19158; Q08239;

T 01-NOV-1990 (Rel. 16, Created)

T 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

E Inhibitory regulator protein IRA2.

GN IRAZ OR GLC4 OR CCS1 OR YOLO81W OR 00985.

OS Saccharomyces cerevisiae (Baker's yeast).

OC ELKaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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SEQUENCE FROM N.A.

MEDLINE-90318397; PubMed-2164637;

Tanaka K., Nakafuku M., Tamanol F., Kaziro Y., Matsumoto Tanaka K., Nakafuku M., Tamanol F., Kaziro Y., Matsumoto Tanaka K., Nakafuku M., Tamanol F., Kaziro Y., Matsumoto Tanaka K., Nakafuku M., Tanaka K., Nakafuku M., Tanaka K., Nakafuku M., Tanaka K., Nakafuku M., N
                                                                                                                                             InterPro; IPR001936; RasGAPfam; PF00616; RasGAP; 1.
SMART; SM00323; RasGAP; 1.
                                                                                                                                                                                                                                                                                                                                 EMBL; M33779; AAA34710.1; -. EMBL; X83121; CAA58201.1; -. EMBL; X75449; CAA53202.1; -. EMBL; Z74823; CAA99093.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a cobeween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tzermia M., Katsoulou C., Alexandraki D.;
"Sequence analysis of a 33.2 kb segment from the left arm of chromosome XV reveals eight known genes and ten new open reac frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags.";
Yeast 13:583-589(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zumstein E., Griffin H., Schweizer M., Sequence of a 10.27 kb segment on the Saccharomyces cerevisiae includes part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1982-3079 FROM N.A. MEDLINE-97321807; PubMed-9178509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae putative new gene."; Yeast 10:1383-1387(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288c / FY
MEDLINE-95208358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-2423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION OF CCS1 AS IRA2.
MEDLINE-92405229; PubMed-1326414;
                                                                                                                                                                                                                  S11190; RGBYI2.
S0005441; IRA2.
rPro; IPR001936; RasGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell. Biol. 10:4303-4313(1990).
       activation.
1701
                                                                    PS00509; RAS_GTPASE_ACTIV_1; PS50018; RAS_GTPASE_ACTIV_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FY1679
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IRA2 gene and a
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RA SQUINGS J., Peat N., Hayles J., Baker S., Basham D., Bownan S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Sauares S., Stevens K.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Vonstreels E., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vanstreels E., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Ger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Best Local
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CONFLICT
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Eukaryota; Fungi; Ascomycota; Schlzosaccharomycetes;

Schlzosaccharomycetales; Schlzosaccharomycetaceae;

Schlzosaccharomyces.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 36, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
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POLY-LEU.
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Matches 61
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Pfam; PF00330; aconitase_C; 1.
Pfam; PF00694; Aconitase_C; 1.
PRINTS; PR00415; ACONITASE_N; 1.
ProDom; PD000511; Aconitase_N; 1.
TICRPAMS; TICR00170; LeuC; 1.
TICRPAMS; TICR00171; LeuD; 1.
PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
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between
the Euro
     VL2_HPV03
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SEQUENCE
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InterPro; IPR000573; Acon:
InterPro; IPR001030; Acon:
InterPro; IPR004430; LeuC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002)
-I- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
-I- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leucine biosynthesis; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H(2)0.
CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS
                                                                                                                  577
                                                                                                                                                                                                                                                              469
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                                                                                                                                                                                                                                                                                                                                   409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                               FAFY----EIRYDADG-
                                                                                                                                               WEFYPLSKQQLQYAATDAYASWHLYKVLKDLPDAV
                                                                                                                                                                                                                                                                             DSNYCDVMHIF---HSGIPQSLQHLIEDSTLVKYGIGIDGDSVKLFHDYGYSIKDVEDL-: |: | | | |:|: | |
                                                                                                                                                                                                                                                                                                                                                                                                           DKVFIGSCTNSRIEDLRLAAAVVKGRKVAANVKDAMIVPGSGLVKKM---AEAEGLDQIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAADVLPTVTWGTSPQDVIPINGNIPDPAHVKDNVRAASIQRSLEYMGLKPNTSIVSYPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDADGIATNVAGSVSSGSAGIPKFTVVEGIAAPLPMANVDTDKIIPKQFLKTIKRTGLGQ
                                                                                                                                                                                                                        --SDLANQKIGGDKKWGLASL----
                                                                                                                                                                                                                                                            KGHLCNVREFFGDVSNGSPSIITNKNYDPS-----HDVEG
                                                                                                                                                                                                                                                                                                                                   IEAGFDWREAGCSMCLGMNPDQLKPYERCASTSNRNFEGRQGAKGRTHLVSPAMAAAAAI
                                                                                                                                                                                                                                                                                                                                                                         VGLDIEWRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leucine biosynthesis; second step.
TY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             -CRARNFPAMREGGRILYSKTATEVDKRAM-----QLIKVLDTKRDESGI--AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 I
420 I
423 I
82782 MW;
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18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iron-sulfur; 4Fe-4S.
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB 1
Pred. No. 4.9;
53; Mismatches
                      PRT;
                      473
                                                                                                               KEIPDFV 595
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1S) (BY
1S) (BY
CRC64;
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                                                                                                                                                                                                                                                            516
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   RESULT 10
CPV1_MOUSE
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Best Local
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01-JUN-1994 (
01-OCT-1996 (
Minor capsid
                                                      synthetase) (P-450AROM). CYP19 OR AROM.
                                                                                                                                                                                  CPV1_MOUSE
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Pfam; PF00513; late_protein_L2;
Coat protein; Late protein.
                  Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X74462; CAA52473.1; -. PIR; S36553; S36553.
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Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                  PDAVSG
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(Rel. 29,
(Rel. 34,
d protein
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ilarity 21.6%;
Conservative 3
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                               366
Chordata;
Rodentia;
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P28649;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 19 (Aromatase) (EC 1.14.14.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSAAPTVQATTSVHGHEEDPNQIPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIG
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. 29, Last sequence upo
. 34, Last annotation u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 91.5; D; Pred. No. 2.9; 34; Mismatches
Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stage;
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ion update)
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Vertebrata;
thi; Muridae;
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                                                                                                                       (CYPXIX)
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                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     types.";
  Murinae;
                                                                                                                       (Estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111;
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Best Local S
Matches 38
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
STRAINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.!
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.!
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D.,
                                                                                                                                                                              P43741;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
POLA OR HI0856.
                                                                                                                                                                                                                                                                                     HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; $13912; $13912.

MGD; MGI:88587; Cyp19.

InterPro; IPR001128; Cytochrome_P450.

Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                   Haemophilus
Bacteria; Pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maeda T., Shizuta Y.;
"Isolation of a full-length cDNA encoding mouse ar
Arch. Biochem. Biophys. 285:231-237(1991).
-1- FUNCTION: CATALYZES THE FORMATION OF AROMATIC
                                                                                                                                                                                                                                                                      DPO1_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Electron transport; Oxidoreductase; Monooxygenase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terashima M., Toda K., Kawamoto
                                                                                                                        NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91378248; PubMed-1897929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxidized flavoprotein + H(2)O.
SUBCELLULAR LOCATION: Membrane-bound.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C19 ANDROGENS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEW----RPSFRKGVL-PGK
                                                                                                                                                     Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
503 AA;
                                                                                                                                                                     influenzae.
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                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437 H
58015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%;
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                                                                                                                                                     gamma subdivision; Pasteurellaceae;
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Pred. No.
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Best Local S
Matches 61
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InterPro; IPR00513; EXC_N_I.
InterPro; IPR005584; HHH_2.
Pfam; PF00476; DNA_POl_A; 1.
Pfam; PF01612; 3__exonuclease; 1
Pfam; PF01612; 3__exonuclease; 1
Pfam; PF01612; 3__exonuclease; 1
Pfam; PF02799; 5_3_exonuc_N; 1.
SMART; SM00474; 35EXOC; 1.
SMART; SM00474; 35EXOC; 1.
SMART; SM00479; HhH2; 1.
SMART; SM00479; HhH2; 1.
SMART; SM00482; POLAC; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00593; policy, ...
PROSTITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 930 AA; 103740 MW; 226654BB7CFF730B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Et the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
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                                KKWGLASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVL
                                                                                 EDSTLVKVGIGIDGDSVKLFHDYGVSIKDVE-----
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IPR002421;
IPR001098;
IPR002298;
                                                                                                                                                               FVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQH------LI
                                                                ENPNIHKIGQNIKFDE-SIFARHGIELQGVEFDTMLLSYTLNSTGRHNMDDLAKRYLG--
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5_3_exonuclease.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Score 89.5;
Pred. No. 11;
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informatics and the EMBL outstation -
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HRSHC_ARATHLE HRSHCLICH HRSHCTLORUGAREA

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RESULT 13 BLM_DROME

BIM_DROME STAN Q9VGI8; Q9V062; 15-JUN-2002 (Rel. 4 15-JUN-2002 (Rel. 4 15-JUN-2002 (Rel. 4

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Matches 68
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InterPro: IPR002863; MutS_N.
InterPro: IPR002863; MutS_N.
InterPro: IPR002999; Tudor.
Pfam; PF00488; MutS_C; 1.
Pfam; PF01624; MutS_C; 1.
PfoDom; PD001263; MutS_C; 1.
SMART; SM00534; MUTSd; 1.
SMART; SM00533; MUTSd; 1.
SMART; SM00533; TUDOR; 1.
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Granat S., Shoh
Chen E., Marra
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CONFLICT
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Shohdy N., Hasegawa A., Hameed A., Lodhi
arra M., Martienssen R., McComble W.R.;
and analysis of chromosome 4 of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1324
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Bioinformatics Institute.
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ADR -> GKPKSLLI.
Q -> QVRRA.
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-> QVRRAHGNL (IN REF. 1).
-> PGIINLLHIHILLILANCTASHIISLP
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RA Abril J.F. Abyler C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Bersova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Botshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dietz S.M., RA Cherry J.M., Carrell J.H., Gu Z., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lin X., Mattel B., McIntosh T.C., McLeod M.P., Ketchum K.A., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., McKalubry G., Milshina N.V., Mobarry C., Morris J., Mosnrefi A., RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Reinert K., Remington K.S., Saunders R.D.C., Scheeler F., Shen H., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Klamos I., Simpson M., Stopski M.P., Smith T., RA Shue B.C., Siden-Klamos I., Simpson M., Stopski M.P., Smith T., RA Shue B.C., Siden-Klamos I., Simpson M., Stopski M.P., Smith T., RA Shue B.C., Sheng T., Weitsenbach J., RA Mang X., Weitsenbach J., Ra Zheng X.H., Zhong F.N., Nelson G.M., Weissenbach J., Ra Zheng X.H., Zhong F.N., Nelson G.M., Stong R., Shue Q., Zheng L., Shith H.O., Ra Zheng X.H., Shith H.O., Ra Cherry S. Shith H.O., Ra Ch
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashbushrar M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Whill, L.D., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Whill T., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Berkeley
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                                                                                                                                                                                                                           FUNCTION: Participates in DNA replication and may participate in repair. Exhibits a magnesium dependent ATP-dependent DNA-helicase activity that unwinds single- and double-stranded DNA in a 3'-5' direction (By similarity).
SUBCELLULAR LOCATION: Nuclear (By similarity).
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
SIMILARITY: CONTAINS 1 HRDC DOMAIN.
                                                                                                                   European Bioinformatics Institute.
                                                                                                                                           SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
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M.E., Engels W.R.;
RECQ family of helicases: a Drosophila homolog,
to the human Bloom syndrome gene.";
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Query Match
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pfam; PF00570; HRDC; 1.
SMART; SM00487; DEXDO: 1.
SMART; SM00490; HELICC; 1.
SMART; SM00414; HRDC; 1.
TIGREAMS; TIGR00614; recq; 1.
PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                            ----YAAT
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RESULT 14

NYZB_BRARE

IN 28_BRARE

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Matches 45
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15-JUL-1999 (Rel. 38, Last
15-JUN-2002 (Rel. 41, Last
Homeobox protein NK-2 homo.
NKX2-2 OR NKX2.2 OR NK2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZFIN: ZDB-GENE-980526-403; nkx2.2.
InterPro; IPR001356; Homeobox.
Pfam; PP00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-95324401; PubMed-7600991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NK2B_BRARE
Q90481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barth K.A., Wilson S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox; DNA-binding; Developmental protein; Nuclear protein

NA_BIND 125 184 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                 162
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P22808; 1NK3.
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                                                                                                  ASLIRLTPTQVKIWFQNHRYKMKRARAEKGMEVTHLPSPRRVAVPVLVRDGKPCHTLKAQ 218
                                                                                                                                                                                                             SNGSDSGKKRKR----
                                                                                                                                                                                                                                                                                                                  DNPYT-RWLATTDSIQYSLHGLSANSQDTSAKSP
                                                                                                                                                                                                                                                                                                                                                                 DDAFTEEELLAIDAIEAS-YNFSRSSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Last annotation update)
homolog B (Homeobox protein
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                                              JHDJSD.
                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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Pred. No. 2.7;
32; Mismatches
                                                                                                                                   -RDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYC
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241
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2.7;
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Best Local
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STRAIN-EI TOR N16961 / Serotype 01;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROA_VIBCH Q9KPT9;
                                                                                                                                                                                                                                                                       TIGRAMS; TIGR00407; proA; 1.

PROSITE; PS01223; PROA; FALSE_NEG.

Oxidoreductase; Proline biosynthesis; NADP; Complete proteome.

OXIDENCE 416 AA; 44504 MW; 7ACA58E537235563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ENthe European Bioinformatics Institute. There are no restructed the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).

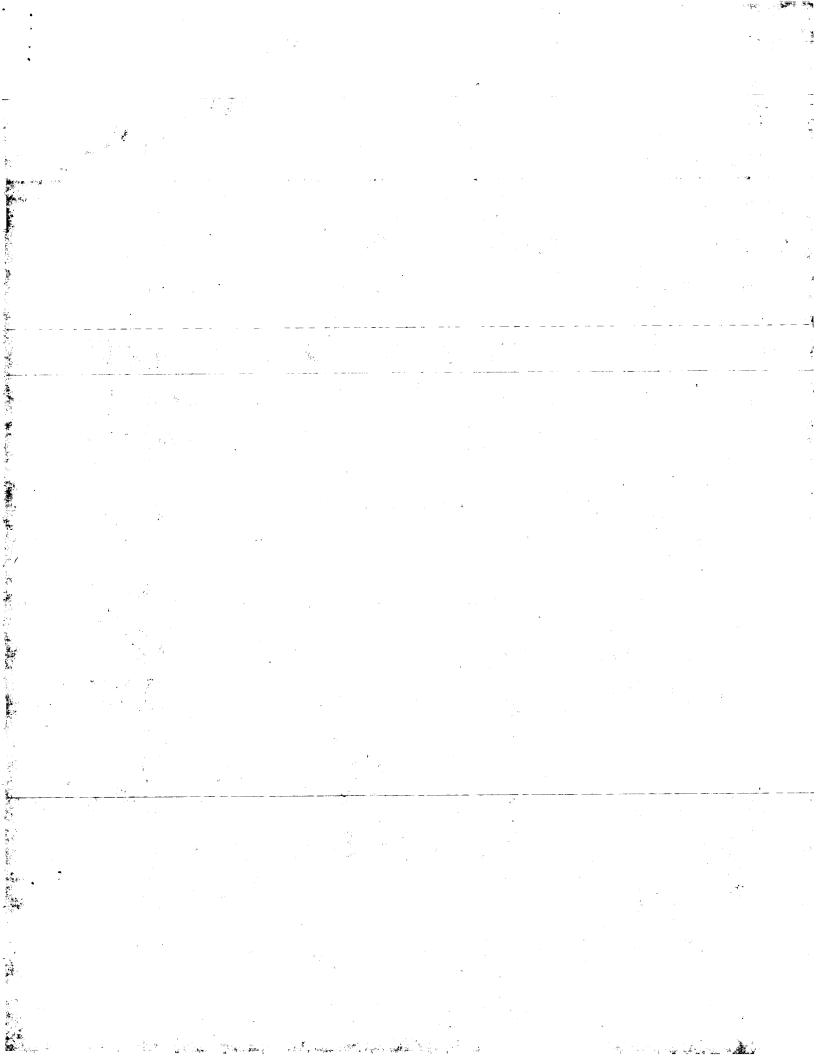
1: FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMPORT FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMPORT SPONTANEOUSLY UNDERGOES CYCLIZATION PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Gamma-glutamyl edhydrogenase) (Glutamyl-gamma-semialdehyde
                                                                                                                                                                                                                                                                                                                                                                                                       TIGR;
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NCBI_TaxID=666;
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PROA OR VC2273.
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002086; A InterPro; IPR000965; G Pfam; PF00171; aldedh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate + NADP(+) = L-gamma-glutamy1 5-phosphate + NADPH.

PATHWAY: Proline biosynthesis; second step.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY.
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159
                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                       AE004299; AAF95417.1; ALT_INIT VC2273; -.
                                                                                                     64
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                                                                                                                                                                           7
                                                                                                                                                                                                             69;
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
VIQSALDKAGLPAASVQYIE----
                                VLDTKRDESGIAFVGLD-IEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQ--
                                                                                                    RQLPRSITSSTSYKRFP-----LSRC-RARNFPAMRFGGRILYSKTATEVDKRAMQLIK 116
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                                                                     RRVPLGVV-GVIYEARPNVTIDIAALCLKTGNAAILRGGKETFFSN---
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                                                                                                                                                                                                         Score 88; DB 1
Pred. No. 4.8;
54; Mismatches
                                                                                                                                        NESRLQAIANDVRNVIKLNDPV-GSEIDSRVLENGMSLAR 108
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KPDRELVTQLLKMDDYVDMI - -
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Search co Job time	В	Qy	DЬ	Qy	Db	Qy
Search completed: June 6, 2003, 10:22:52 Job time : 12 secs	312 WLSYTLGVKVVQDVQEAI 329	272 WHLYKVLKDLPDAV 285	252 SACNALDTLLVHQAIAKPLLDKLIAKLNGKVAFVAEPKAKALMSSAAELRDAQAGDFDTE 311	226 WGLASITETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYAS 271	204 AGLHKMCKENSTVPVIIGGFGISHIFVDESADLDKSVAVIENAKVQRP 251)GDSVKLFHDYGVSIKDVEDLSDL



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Listing first 45 summaries
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Gapop 10.
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Copyright (c) 1993 - 2003 Compugen
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sp_unclassified:*
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                Q9ft68 arabidopsis
Q9svm6 arabidopsis
Q9svm6 arabidopsis
O93530 xeenopus lae
Q9z241 mus musculu
Q9jk04 mus musculu
Q35948 mus musculu
Q3vu9 oryza sativ
Q9ve86 drosophila
Q8z2j5 oryza sativ
Q9fele1 drosophila
Q9vgn7 drosophila
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6.3	6.3	6.4	6.4	6.4	6.5		6.5	6.5	6.6	6.6	6.6		6.8	6.9	6.9	7.0	7.2	7.4	7.4	7.4	7.5	7.5			9.5	10.1	10.2	10.2
416	353	4589	925	455	488	906	579	445	216	532	265	393	876	710	220	625	300	238	300	242	210	217	505	239	599	496	199	496
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096144	Q9LHG4	076506	Q9GUG1	Q9ZWS2	Q97JZ0	Q17281	Q9RQK2	Q9YDV0	Q8SA46	Q976Y3	Q9LHG5	Q8R7C1	Q17951	Q9NA69	Q9LHG1	Q9VIF1	Q8RNV0	Q9C7A5	Q9AL74	Q9LHG2	Q9LHG3	080886	Q9FIN8	Q9SIH3	Q96NP1	Q9NVH0	Q9LK79	Q8VEG4
096144 plasmodium	4	076506 tetrahymena	0	Q9zws2 vigna mungo	Q97jz0 clostridium	Q17281 botryllus s	ь	Q9ydv0 aeropyrum p	Q8sa46 hordeum vul	Q976y3 sulfolobus	Q91hg5 arabidops1s	Q8r7c1 thermoanaer	Q17951 caenorhabdi	0	Q9lhg1 arabidopsis	Q9vif1 drosophila	Q8rnv0 citrobacter	Q9c7a5 arabidopsis	Q9al74 citrobacter					3 arab	Q96np1 homo sapien	homo	Q91k79 arabidopsis	Q8veg4 mus musculu

ALIGNMENTS

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RESULT 1
Q9FT68
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Best Local S
Matches 285
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Q9FT68; O1-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN.2002 (TrEMBLrel. 21,
                                                                                                                                                              Nucleic Acids Res. 21:4275-4282(2000).
EMBL; AJ404476; CAC14871.1; -.
InterPro; IPR002562; 3__exonuclease.
Pfam; PF01612; 3_exonuclease; 1.
SMART; SM00474; 35EXOC; 1.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=COLUMBIA; TISSUE=FLOWER;
Hartung F., Plchova H., Puchta H.;
Molecular characterisation of RecQ homologues
                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                         WRNEXO
                                                                                                                                                                                                                                                                                                                                                                                     Exonuclease.
                                                                                                                                                                                                                            thaliana.";
61
            61 NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120
                                                                                                              Similarity
                                                NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
                                                                                                                                                    285 AA;
                                                                                                    Conservative
                                                                                                                                                    31750 MW; A198CB93653E229B CRC64;
                                                                                                            98.48;
                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                 0;
                                                                                                             Score 1466.5;
Pred. No. 6.7
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es 0; Indels
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                                                                                                                                                                                  Query Match
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01-JUN-2001 (TIEMBLIEL 17, Last annotation
Hypothetical 35.1 kDa protein.
F18A5.260 OR AT4G13870.
Arabidopsis thalfan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 313 AA;
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bmitted (MAR-2000) to the EMBL/GenBank/DDBJ
BL; ALO35528; CAB36851.1; -.
BL; AL161537; CAB78429.1; -.
terPro; IPR002562; 3_5_exonuclease.
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; SM00474; 35EXOC; 1.
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DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL
          DSTLYKYGIGIDGDSYKLFHDYGYSIKDVEDLSDLANQKIGGDKKWGLASLTETLYCKEL
                                                        KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE 180
                                                                                                    NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
                                                                                                                                                 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSAAPTVQATTSVHGHEEDPNQIPN
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                                             KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE
                                                                                          NIRRQLPRSITSSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
                                                                                                                                    MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSAAPTVQATTSVHGHEEDPNQIPN
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                                                                                                                                                                                            Score 1439.5; DB 1
Pred. No. 1.8e-118;
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                                                                                                                                                                                                                             448D7ACC375D4D22 CRC64;
                                                                                                                                                                                  Mismatches
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01-NOV-1998
01-NOV-1998
01-JUN-2002
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NP_BIND
SITE
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SMART; SMO
TIGRFAMS;
Hydrolase;
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SMART;
SMART;
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InterPro;
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                                                                                                                                                                                                SEQUENCE
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-1- SIMILARITY: BELONGS TO THE RECQ SUBFAMILY OF HELICASES
-1- SIMILARITY: CONTAINS 1 HRDC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96032793;
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MEDLINE-98361165; PubMed-9697700;
Yan H., Chen C.-Y., Kobayashi R., Ne
"Replication focus-forming activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                              Local
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m; PF00270; DEAD; 1.
m; PF00270; Helicase_C; 1.
m; PF00570; HRDC; 1.
RT; SM00474; 35EXOC; 1.
RT; SM00479; HELICC; 1.
RT; SM00490; HELICC; 1.
RT; SM00341; HRDC; 1.
RT; SM00341; HRDC; 1.
RT; SM00341; HGDC; 1.
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82; Conserv
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KRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIF-
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                                                                                       NIRROLPRSITSSTSYKRF---PLSRCRAR----NFPAMREGGRILYSKTATEV-----D
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8 (TrEMBLrel. 08, Last s
2 (TrEMBLrel. 21, Last a
drome helicase homolog (
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nilarity 35.0%;
Conservative 4:
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POLY-ASP.
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ATP (BY ST
DEAH P'
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                                                                                                                          Score 339.5; DE Pred. No. 8e-21; Mismatches
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ייחing activity 1
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H BOX.
1BEAF05A25B4E230
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Pipidae;
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Matches 74
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Q9JKD4;
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Pfam; PF00271; helicase_C;
SMART; SM00474; 35EXOc; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Z241;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TI
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF091216; AAC7; InterPro; IPR002562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF091216; AAC72359.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paeper B.W., Gayle M., Brady W., Mulligan J., Galas D., Fu Y.-H.; "Genomic structure of the human I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Z241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IP
Pfam; PF0161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nomolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                         AATDAYASWHLYKVLKDLPDAV
                                                                                                                                                                                                                                                                                                                                                             K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                                                                                                                                                                                                                                                              VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGLIKHLFKEQLYKRKSYRCSNWDIFLLTEDQKLYAATDAYAGLLIYKKLEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKYLKDL
                                                                                                                                                                                                                                                        VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                                        KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                                                                                                                                                                                                                                      NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATDAYAGLIIYQKLGNLGDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00490; HELICC; 1.
TIGR00614; recq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR004589; RecQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              886
    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicase.
                                                                  PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.7%;
36.6%;
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    15,
15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 339; DB
Pred. No. 5.3e
42; Mismatches
  Created)
Last sequence update)
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Last annotation update)
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                                                                PRT;
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                                                                1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
5.3e-21;
hes 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α:,
                                                                A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 988;
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Best Local S
Matches 74
                                                                                                                                                                                                           035948;
01-JAN-1998
01-JAN-1998
01-JUN-2002
SEQUENCE FROM N.A. Wu J., He J., Mour "mouse WRN.";
                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00271; helicase_C; 1.
pfam; PF00570; HRDC; 1.
SMART; SM00474; 35EXOC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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MO1. Cell. Biol. 20:3286-329

EMBL; AF241636; AAF64490.1;

MGD; MGI:109635; Wrn.
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MEDLINE-20221574; PubMed-10757812;

Lombard D.B., Beard C., Johnson B., Maronson R., Buhlmann J.E., Lipman R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                               035948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
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                                                                                                                                                                    WRN OR WRN
                                                                                                                                                                                       Homolog of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGRO0614; recq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090
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PF00270;
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SM00341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 36.0
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  AATDAYAGLIIYQKLGNLGDTV
                                                                                                                                                                                                                                                                                                                                                                                                                        AATDAYASWHLYKVLKDLPDAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFPAMREGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSERKGVLPG
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IPR004589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002562;
IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g; Helicase.
1401 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; S
                                                                                                                                                                                     (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence up
(TrEMBLrel. 21, Last annotation
human Werners syndrome protein.
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guarente
                       Mountz
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                     J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.7%;
36.6%;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 339;
Pred. No. 8.
                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                                                                           285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
8.5e-21;
hes 72;
                                                                                                                                                                                                                              update)
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                                                                                                                           Euteleostomi;
                                                                                                         Murinae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q93VU9 PRELIMINARY; PRT; 201 AA.
Q93VU9;
Q93VU9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 20, Last annotation update)
Q1-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-NAR-2002 (TrEMBLrel. 30, Last sequence update)
Q1-NAR-2002 (TrEMBLrel. 19, Created)
Q1-NAR-2002 (TrEMBLrel. 19, Last sequence update)
Q1-NAR-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
SASAKI T., MATSUMOOTO T., YAMAN
"Oryza sativa nipponbare(GA3)
clone:P0487H02.";
                                                                                                                                                                              Submitted (MAY-2001) to the EMBL; AP002883; BAB67862.1; EMBL; AP003578; BAB60933.1;
                                                                                                                                                                                                                                                                         STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki tativa nipponbare(GA3) genomic
clone:P0682B08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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EMBL; U97045; AA
MGD; MGI:109635;
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
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n; PF00271; helicase_C; 1.
rr; SM00474; 35EXOC; 1.
rr; SM00490; HELICC; 1.
rr; SM00490; HELICC; 1.
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Pro; IPR004589; RecQ
PF01612; 3_5_exonuc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSTOHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANOKIGGDKKWGLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLQRKFPEWMSMQSQRCATEEKACVQKNVLEDNLPFLEFPGSIVYSYEASD----CSFLS
                                                                                                                                                     IPR002562; 3_5_exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001410;
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                                                                                          _5_exonuclease;
A; 21899 MW;
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   16.0%;
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Score
Pred.
                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
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Pred. No. 1.
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   238;
No. '
                                                                                                                                                                                                                                                                                                        DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA,
   4.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7e-20;
hes 83;
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                                  201;
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          RX MEDLINE-20196006; PubMed=10731132;
RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J. Brokstein P., Bothier P.,
RA Borkova D., Botchan M.R., Bouck J. Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J. Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evanqelista C.C., Ferriara S., Fleischannn W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gdan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gdan P., Harris M.,
RA Glodek A., Gong F., Marrey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Karft C., Kravitz S., Kulp D., Lai Z.,
RA Munt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Munt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixoff K., Nusskern D.R., Pacleb J.M.,
RA Holton S.M., Wooday F.N., Zhong M., Skipski M.P., Smith T.,
Shen B. S., Kodella R., Shen B., Shen H.,
Shen B., Mang S., Yao Q.A., Nang S., Zho Q., Zheng L.,
RA Globes R., Packer J.S., Zhan M., Zhang G., Zhao Q.A., Maith H.O.,
RA Che
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01-MAY-2000
01-JUN-2001
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY;
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   X.H.,
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   Zhong
Myers
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 E.W.
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13,
17,
   Zhong W., Z
Rubin G.M.,
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a; Brachycera; Musc
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Best Local S
Matches 58
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:OSJNBbD021A09.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003218; BABB9458.1;
-SEQUENCE 501 AA; 56404 MW; 153AB72F4064FA99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8S2J5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Pfam; PF01612; 3_5 exonuclease; 1.
SMART; SM00474; 35EXOc; 1.
SEQUENCE 346 AA; 39398 MW; 3150A9
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FlyBase; FBgn0038608; CG76
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nce 287:2185-2195(2000).
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     GLVREVMGVWAPKPYHVRVSAWDSWNLTPEQVMYACADAFASF
                                    SLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASW
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                                                                                                                                                                                                                                                                                                                           15.3%; Score 227.5;
35.6%; Pred. No. 1.40
Live 28; Mismatches
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Last sequence update)
Last annotation updat
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Pred. No. 5.5
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hes 123;
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OF CALL
RESULT 11

Q9VGN7

ID 09VGN

AC 09VGN

AC 09VGN

DF 01-MA

DF 01-JU

DE CG674

GN CG674

GN CG674

OS Droso

OC Eukar

OC Phery

OC Phery

OC EPhylor

CG PHOL

RN [1]

RP SEQUE

RX MEDLLI
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Query Match
Best Local S
Matches 65
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Q9VGN7;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAR-2001 (TrEMBLrel. 16, L
O1-JUN-2002 (TrEMBLrel. 21, L
CG6744 protein (AT25352p).
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01-DEC-2001
01-DEC-2001
01-MAR-2002
GM14514p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J. Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J. Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY051647; AAK93071.1; -

EMBL; AY051647; AAK93071.1; -

EMBL; BY001808; CG7670.

InterPro; IPR002562; 3_5_exonuclease.

Fiam; PF01612; 3_5_exonuclease.
SEQUENCE FROM N.A. STRAIN-BERKELEY; MEDLINE-20196006;
                                                                       Ephydroidea; Drosophilidae; NCBI_TaxID=7227;
                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTESQDIAASADDVLQWVEKQKAE--VVPMAFDMEWPFSFQTG---PGKSAVIQICVDEKC
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                                                                                                                                                                                                                                                                                                                                                                                        312
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 PubMed-10731132;
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19,
20,
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Last annotation updat
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3; Mismatches
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                                                                                                                 Brachycera; Muscomorpha;
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RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Barer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Duck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dew II., Dletz S.M.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dev II., Dletz S.M.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dev II., Dletz S.M.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dev II., Dletz S.M.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Diegwam C.,
RA Jalali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Harris N.L., Moy M., Murphy B., Murphy L., Muray D.M., Nelson D.L.,
RA Merkilvo G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Merkilvo G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Merkilvo G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Merkilvo G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Pacleb J.M.,
RA Ranger E.C., Stapleton M., Strong R., Sun E.,
RA Sylreks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Sylreks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Harris R.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Libas R.A., Werse S. M., Welsen D., Zhu
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Best Local
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                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
               280
                                                   167
                                                                                                                        109
                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                            Similarity
_ 무
                                                                            GGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLY-KVLK
                                                                                                                    DVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI
                                                 AGHKPEGLGKLSKTHLNYTLDKHWRLACSNWEAKTLEPKQLDYAANDALMAVAIYQKLCR
                                                                                                                                                                                                                                   KRAMQLIKVLDTKRDESGIAFVGLDIEW------RPSFRKGVLPGKVATVQICVDSNYC
                                                                                                                                                                                                                                                                                                                                                 583 AA;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                 66866 MW;
                                                                                                                                                                                                                                                                                        14.3%;
                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                        Score 212.5;
Pred. No. 3.
                                                                                                                                                                                                -GFDCEWITVGGSRRP------VALLQLSSHRGLC
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les 65;
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Kim C.J., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nuyuen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
Teguence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9C7K6;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002562; 3_5_exonuclease.
InterPro; IPR002114; HPr_SerP_site.
Pfam; PF01612; 3_5_exonuclease; 1.
SMART; SM00474; 35EXOc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidonsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).
EMBL; AC069159; AAG50917.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21016719: PubMed=11130712:
Theologis A., Ecker J.R., Palm C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
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549
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                                 281
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                  GIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSN--YCDVMHIFHSG---IPQSLQHLIE 180
                               LPDAVSGS
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                                                                                                       GGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKD
                                                                                                                                          SKSTLKLVSLTEDYPDHKLSSGYNFQCDIKQLALSYG-DLKCFERYDMLLDIQNVFNEPF
                                                                                                                                                                                                                GCRVVGIDCEWKPNYIKGSKQNKVSIMQIGSDTKIFILDLIKLYNDASEILDNCLSHILQ 436
HPPHDSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                         582 AA;
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                                                                                                                                                                                                                                                                                      Conservative
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                                                                      -GLAGLTKKILGVSLNKTR--RNSDWEQRPLSQNQLEYAALDAAVLIHIFRHVRD
                                   288
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                                                                                                                                                                                                                                                                                                                                                         66467 MW;
                                                                                                                                                                                                                                                                                                     12.0%;
                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                    Score 179.5;
Pred. No. 2.8e
36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         34D752473F786680 CRC64;
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RESULT 13 Q8SA18 ID Q8SA18

PRELIMINARY;

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PROPERTY OF THE PROPERTY OF TH
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Best Local S
Matches 53
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Q1-JUN-2002 (TrEMBLrel.:

O1-JUN-2002 (TrEMBLrel.:

O1-JUN-2002 (TrEMBLrel.:

P0684E06.27 protein.:

P0684E06.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          037VS2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01487H02.21 protein (P0682B08.2 protein).
01722 sativa (Rice).
01722 sativa (Rice).
01723 sativa (Rice).
01724 sativa (Rice).
01725 sativa (Rice).
01725 sativa (Rice).
01726 sativa (Rice).
                    Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AP002883; BAB67861.1; EMBL; AP003578; BAB60932.1;
                                                                                                            STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
**Oryza sattva nipponbare(GA3) genomic
clone:P0682808.*;
                                                                                                                                                                                                                                                                                                           STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Mpponbare(GA3) genomic
clone:P0487H02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q93VS2
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Sasaki T., Matsumoto T., Yamam
"Oryza sativa nipponbare(GA3)
clone:P0684E06.",
clone:P0684E06."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL, AP003291; BAB85281.1;
  InterPro;
                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4530;
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  IPR002562;
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Last sequence update)
Last annotation update)
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Query Match
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Best Local :
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01-JUN-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
EMBL; AL513443; CAC28658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt
Nyakatura G., Mewes H.W., Mannhaupt G.;
                                                                                                                                                                                                                                                                                                                           InterPro; IPR002562; 3_5 exonuclease. Pfam; PF01612; 3_5 exonuclease; 1. SMARP; SM00474; 35EXOC; 1. SMARP; SM00474; 35EXOC; 1. SMARP; SM00474; 37EXOC; 1. SMARP; 42FE96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Related to WERNER syndrome 93G11.60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycot
Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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QQLQYAATDAYASWHLYKVL
                                GIYELSHLYKLVKYSASGEHKLVNRRLVPLATLVKEVLQLPMFK-GAVRTSEWS-KPLNM
                                                                      DVEDLSDL ---
                                                                                                                           VDSNYCDVMHIFHSGI-PQS------LQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIK
                                                                                                                                                                            KVHYCRSATTTERVLKQYF--MDEK------ILGLDLEWEISAKESHGPRQNVSVIQIA
                                                                                                                                                                                                 RILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGK-VATVQIC:: | :: | :: | :: | : |: :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
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24.3%; Pred. No. 7.5;
tive 42; Mismatches
                                                                    -ANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSK
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                                                                                                                                                                                                                                                   Score 159.5; DB 3;
Pred. No. 2.1e-05;
2; Mismatches 73;
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7.5e-07;
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Search completed: June 6, 2003, 10:24:14 Job time: 35 secs

Sequence 12, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli Sequence 11, Appli Sequence 7, Appli

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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length: 2000000000
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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   US-08-781-891-71
US-09-127-670-6
US-09-127-670-6
US-08-781-891-206
PCT-US94-00108-4
US-09-134-001C-5314
US-09-721-832-2
US-09-721-832-2
US-09-721-835-2
US-07-989-85-72
US-08-987-367-2
US-08-987-367-2
US-08-987-367-2
US-08-997-166-12
US-08-990-713-4-001C-4528
US-08-990-713-34
US-08-895-601-6
US-09-138-743-34
US-09-138-743-14
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564.920 Million cell updates/sec
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Compugen Ltd.
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US-08-781-891-71
                                                                                                                       TOPOLOGY: US-08-781-891-71
                                                                                                                                                                                               APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Ca
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.41
TELEPHONE: (206) 622-4900
TELEPAN: (206) 682-6931
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                   Query Match
Best Local S
Matches 75
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Patent No. 609063
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APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Willigan, John T.
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                        OPEKALLING CONTROL OF THE PROPERTY APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/781,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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CITY: Seattle
STATE: Washington
                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
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ZIP: 98104-7092
                                                                                                                                                                                          LENGTH:
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75; Conserv
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                                                     Conservative
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                                                  23.6%; Score 352; DB 3; 37.7%; Pred. No. 8.3e-30; bive 41; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version #1.30
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US-08-439-992A-2
US-08-323-430-12
US-09-216-295-8
US-09-216-295-8
US-09-2171-438A-11
US-09-132-028-2
US-08-687-289A-7
US-08-687-289A-8
US-08-687-289A-8
US-08-485-568-7
US-08-486-7513-7
US-08-484-7519B-7
US-08-484-719B-7
US-08-484-159-7
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Gaps

Minimum DB Maximum DB

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Scoring table: Sequence: Perfect score:

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RESULT 3
US-08-781-891-206
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US-09-127-670-6
                                                                                                                                                                                      Sequence 206, Application US/08781891 Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6
LENGTH: 1401
GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui

APPLICANT: Vu, Chang-En

APPLICANT: Oshima, Junko

APPLICANT: Mulligan, John T.

APPLICANT: Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

TITLE OF INVENTION: WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ASSAYS FOR COMPOUNDS WHICH TITLE OF INVENTION: SPAN FILE REFERENCE: MIT-7720A CURRENT APPLICATION NUMBER: US/09/127,670 CURRENT FILING DATE: 1998-07-31 EARLIER PELICATION NUMBER: US 60/054,629 EARLIER FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Massachusetts Institute
APPLICANT: Leonard P. Guarente
APPLICANT: David A. Sinclair
APPLICANT: David B. Lombard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
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Pred. No. 2.2e-28;
12; Mismatches 72; Indels 1
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                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application PC/TUS9400198 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1401 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 6.0.8
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering Corp.
STREET: 1 Girald Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Co
CITY: Seattle
STATE: Washing
  APPLICATION
                                                                                                                                                             COUNTRY:
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les 72; Conserv
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                                                                                                                                                                                                          Madison
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)GY: linear
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                                                                                                                                                                                                                                                                                                        Schering Corp.
VENTION: RAS Associated GAP Proteins
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NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.1%;
PCT/US94/00198
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Pred. No. 2.3e-27;
Pred. No. 2.3e-27;
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Gaps

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FILING DATE:

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FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEG ID NOS: 5674

SEQ ID NO 5314

LENGTH: 930
                                                                        ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5314
                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-001C-5314; Sequence 5314, Application US/09134001C; Patent No. 6380370
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Query Match 6.0%;
Best Local Similarity 23.6%;
Matches 71; Conservative 4!
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Best Local
                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (201)822-703: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
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LENGTH: 3079 amino acids
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TELEPHONE: (201)822-7255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/004,824
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX
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 45;
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Pred. No.
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Score 89; DB 4;
Pred. No. 0.84;
5; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 112;
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 117;
                                   Length 930
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Indels
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68;
Gaps
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US-09-722-139-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
APPLICANT: Freedman
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 1055
CURRENT APPLICATION NUMBER: US/09/722,139
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 13
TYPE: PRT
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1188
                                                                      1143
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                                                                                                                                                  1096
                                   281 LPDAV 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 5.9%; Score 87.5; D Similarity 19.0%; Pred. No. 2.3; Second 2.3; Conservative 52; Mismatches
IPDLV 1192
                                                                                                                                                  LMDARINAYIEEEVQRRLQDLHRVISEGCSTSADTMK--
                                                                                                                                                                                                                        EAE-QEALEKDQERLEYEIQQLKQKIYEVDGVQKDHHGTLEGKVASSSLPVSAEKSHLVP 1095
                                                                                                                                                                                                                                                              DIEWRPSFRK-----
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                                                                      QRKLKY---ELCRDLLCVLMPEPDAAACAN---HPLLQQDLVQLSLD----WK-----TE
                                                                                                                                                                                   I----FHSGIPQSIQHLIED-STLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI 220
                                                                                                           GGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKD 280
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                                                        ; ORGANISM: Human US-09-721-689-2
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GENERAL INFORMATION: Beraud, Christophe APPLICANT: Freedman Pintone
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
Query Match
Best Local Similarity
                                                                                                                         SEQ ID NO 2
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SEQ ID NO 2
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Patent ฟัง. 6440685
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                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/721,689
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.4
                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 105
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CURRENT FILING DATE: 2000-11-24
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ORGANISM: Human
                                                                                                         ENGTH:
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   Score 87.5; DB 4; Pred. No. 2.3;
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               Query Match
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                                                                                                                                      TELEX: 910/371-
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US, FILLING DATE: 19921120 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                       TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Swartz, James TITLE OF INVENTION: METH TITLE OF INVENTION: PROD
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                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Generative
                                                                                   TYPE: AMINO ACID
                                                                                                                                              TELEFAX: 415/952-950
TELEX: 910/371-7168
                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                       NAME: Hasak, Janet E. REGISTRATION NUMBER:
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South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94080-4990
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                                                                                                                                       ID NO:
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5.8%;
20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION IN BACTERIAL CELLS
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                                                                                                                                                                                                                                      28,616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 Kb floppy disk
 Score 86.5;
Pred. No. 0.
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   DB 1;
                 Length 348;
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Best Local Similarity

QY 86 ARNFPAMREGGRILYSKTATEV	Query Match 5.8%; Score 86.5; DB 5; Length 348; Best Local Similarity 20.9%; Pred. No. 0.34; Matches 54; Conservative 34; Mismatches 73; Indels 97; Gaps 12;	TELEX: 910/371-7168 ; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 348 amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; COPOLOGY: linear	; ATTORNEY/AGENT INFORMATION: ; NAME: Hasak, Janet E. ; REGISTRATION NUMBER: 28,616 ; REFERENCE/DOCKET NUMBER: 752 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 415/225-1896 ; TELEPHONE: 415/225-1896	CLASSIFICATION: CLASSIFICATION DATA: APPLICATION NUMBER: FILING DATE:	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: patin (Genentech) ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: PCT/US93/11298	; 21F: 94080 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk ; COMPUTER: IBM PC compatible	h San Francisco ifornia SA	CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd	; APPLICANT: Genericech, Inc. ; APPLICANT: Genericech, Inc. ; TITLE OF INVENTION: METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION IN ; TITLE OF INVENTION: BACTERIA ; NUMBER OF SEQUENCES: 31	RESULT 10 PCT-US93-11298-2 ; Sequence 2, Application PC/TUS9311298	Qy 268 AYASWHLYKVLKDLPDAV 285 : Db 321LPDSV 325	QY 214 DIANQKIGGDKKWGIASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATD 267	Db 223 -YAKQNNLAYTKLISADGKPVSPTEENFANAAKGADWSKTFAQ 264	159 NYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLS	Qy 127 IAFVGLDIEWRPSFRKGV	107 AVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVV-RRADGSG	Matches 54; Conservative 34; Mismatches 73; Indels 97; Gaps 12; Qy 86 ARNFPAMRFGGRILYSKTATEV
QY 81 LSRCRARNFPAMREGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSF 140 :	Query Match 5.8%; Score 86.5; DB 4; Length 480; Best Local Similarity 22.1%; Pred. No. 0.56; Matches 43; Conservative 32; Mismatches 63; Indels 57; Gaps 9;	INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 480 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear US-08-987-367-2	; ATTORNEY/AGENT INFORMATION: ; NAME: Jones, Phil B.C.; ; REGISTRATION NUMBER: 38,195 ; REFERENCE/DOCKET NUMBER: 750027.404 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (206) 622-4900	SUFTMARE: PACENTIN MELEASE #1.0, VETSION #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/987,367 ; FILING DATE: 10-DEC-1997 ; CLASSIFICATION:	ADABLE FORM: FPE: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS	CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104	nd SS	; AFFLICAMY: 21019, Gain Tudii ; TITLE OF INVENTION: PLANT URIDINE DIPHOSPHATE-GLUCOSE ; TITLE OF INVENTION: DEHYDROGENASE GENES, PROTEINS, AND USES THEREOF . NUMBER OF SECTEMOTES: 5	APPLICANY: WITCHEY, DEFIICK APPLICANT: Sims, Lynne APPLICANT: Sims, Lynne APPLICANT: Lu, Guihua APPLICANT: Lu, Guihua	CANT: Nichols, CANT: Dhugga, I CANT: Singletan CANT: Saunders	US-08-97-367-2 US-08-97-367-2 ; Sequence 2, Application US/08987367 ; Patent No. 6399859 ; GENERAL INFORMATION:	321	QY 268 AYASWHLYKVLKDLPDAV 285	265 DLTNOKGEDAWPITSTTFILIHKDOKKPEQGTEVLKFFDWAYKTGAKQANDLDYAS	Db 223 -YAKQNNLAYTKLISADGKPVSPTEENFANAAKGADWSKTFAQ 264 OY 214 DLANOKIGGDKKWGLASLTETLVCKELLKDNRIRLGNWEFYPLSKQQLQYAATD 267	NYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLS	Qy 127 IAFVGLDIEWRPSFRKGVLPGKVATVQICVDS 158

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US-08-987-367-4
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                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: JONES, Phill B.C.
REGISTRATION UNMBER: 38,195
REFERENCE/DOCKET NUMBER: 7500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 10-DEC-19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhong, Gan-Yuan
TITLE OF INVENTION: PLANT URIDINE DIPHOSPHATE-GLUCOSE
TITLE OF INVENTION: DEHYDROGENASE GENES, PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                     Local Similarity
                                                                                                                                                                                                               TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Washington
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                                                                                                                                                                                                                                          LENGTH:
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                            141 RKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFH 200
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                                                          58 VKQCRGRN-----LFFS---TDVEKHVA------EADIIFVSVN---TPTK
                                                                                        81 LSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSF 140
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   TRGLGAGKAA----
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                                                                                                                                                                                                                                             480 amino acids
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Dhugga, Kanwarpal S.
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21.5%;
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   -DLTYWESAARMIADVSKSDKIVVEKST--
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Pred. No. 1.6;
32; Mismatches
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                                                                                                                       64;
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; ORGANISM: Aquifex pyrophilus US-08-907-166-12
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US-08-907-166-12
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US-09-134-001C-4528
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 574
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4528
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08907166 Patent No. 5948666
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                                                                                                                                                                                                                                                                                      APPLICANT: Callen, Walter
APPLICANT: Mather, Eric
TITLE ON INCENTION ISOLATION AND IDENTIFICATION
FILE REFERENCE: 09010/027001
CURRENT APPLICATION NUMBER: US/08/907,166
CURRENT FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 333
TYPE: PRT
170 GIPQSIQHLIEDSTLVKVGIGIDGDSVKLF------HDYGV----SIKDVEDLSDLANQK-|: :::: | |:| | | | |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 IYKRLLTKIDE-PENLVIIGDSAGGQIALAFAQM-----LKKEQLSQPGHIVLISPVL 214
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                                                            1 Similarity 21.9
33; Conservative
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                                                                               5.4%;
21.9%;
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Pred. No.
                                                                                 Score 80; I
Pred. No. 3
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                                                              Mismatches
                                                                               3.9;
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                                                                                                       Length
                                                              Indels 40;
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US-08-845-258-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/845,258
FILING DATE: 24 APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: AND TREATM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
114 ELSVKCIIMGAGITASDLNLKGLGFISPDKQST-NVC---NYFEDMHESYHILDTQRASD 169
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                                                                                                                                                    SNIIWVVHSDVIMKRF---NCKNR-----KSLSTHSLTEND-----ILKFGRI 113
                                                                                                         ESGI--AFVGLDIEWRPSFRKG---VLPGKVATVQICVDSNVCDVMH-IFHSGIPQSLQH 177
                                                                                                                                                                           S-----ITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRD 123
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                                                                                                                                                                                                                                                                                                                                           Length 431;
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Search completed: June 6, 2003, 10:24:59
Job time: 17 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                Score
        seq length: 0 seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1491
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       Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                  : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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       DB
       US-10-174-363-22
US-10-2741-669-380
US-09-781-669-380
US-10-268-441-14
US-09-8815-242-12306
US-09-886-615-74
US-09-886-615-74
US-09-738-626-6900
US-09-738-626-6905
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US-10-115-563-14
                  US-09-286-488-34
US-09-737-178-34
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US-09-920-346-2
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1415.867 Million cell updates/sec
sequence 22, Appl
sequence 15, Appl
sequence 11, Appl
sequence 14, Appl
sequence 12306, A
sequence 213, Appl
sequence 6900, Ap
sequence 500, Appl
sequence 50, Appl
sequence 12, Appl
sequence 12, Appl
sequence 12, Appl
sequence 34, Appl
sequence 34, Appl
sequence 6, Appli
sequence 6, Appli
                                                                                                                                                                                          Sequence 14, Appl
Sequence 11133, A
Sequence 2, Appli
Sequence 22, Appl
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7964 7968 822 393 396 11078 11078 11078 11078 3782 3782 3782 3782 3782 3782 3782 37	733 927
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US-09-925-302-714 US-10-977-130-5 US-09-801-388-384 US-09-757-415A-2 US-09-757-415A-2 US-09-815-242-11856 US-09-864-761-43232 US-09-823-394-2 US-10-125-778-28 US-10-125-778-28 US-10-125-778-28 US-10-125-778-28 US-09-727-205-2 US-09-861-846-4 US-09-981-384B-4 US-09-981-289-4 US-09-981-289-4 US-09-981-289-27 US-09-932-297-27 US-09-932-297-27 US-09-934-277-21 US-09-815-242-4959 US-09-815-242-10803 US-09-816-494-2 US-09-964-277-2	US-10-097-534-16 US-10-097-534-15
Sequence 714, App Sequence 5, Appli Sequence 384, App Sequence 11856, A Sequence 21856, A Sequence 43232, A Sequence 28, Appli Sequence 28, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 2459, Appli Sequence 29, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 23, Appli Sequence 22, Appli Sequence 23, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli	Sequence 16, Appl Sequence 15, Appl

ALIGNMENTS

RESULT 1 US-09-729-674-279

Sequence 279, App Patent No. US2001

Application US/09729674 20010039335A1

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward

APPLICANT: APPLICANT:

Collins-Racie, Lisa Evans, Cheryl

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Merberg, David Treacy, Maurice

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SEQ ID NO 279
LENGTH: 147
TYPE: PRT
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Best Local 9
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APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND
FILE REFERENCE: 6055-64X
                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 283
                                                                                                       Local Similarity 35.0
                                                        171 IPQSLQHLIEDSTLVKYGIGIDGDSVKLFHDYGYSIKDVEDLSDLA-----NQKIGGDKK 225
226 WGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLP 282
                                   23 LPRTLLDILADGTILKVGVGCSEDASKLLQDYGLVVRGCLDLRYLAMRQRNNLLCNG--- 79
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                                                                                                   10.1%; Score 151; DB 10; 35.0%; Pred. No. 1.7e-07; tive 20; Mismatches 48;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: ;
US-10-115-563-14
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US-10-115-563-14
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                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             Local
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APPLICATION NUMBER: US/08/410,488
FILING DATE: 24-MAR-1995
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ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN
C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
AND COMPOSITIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 449.0 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Griffin, John H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    126 ASYLDHTFPAEKM--DDAVAPGREYTYEWSISEDSGPT-----HDDPP--CLTHIY
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                                                                                                                                                                                                                                                                                                      h 6.2%;
Similarity 19.2%;
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                                                                                      IEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLT-----
                                                                                                                                                             ESGIAFVGLDIEWRPSFR-----KGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHL 178
                                                                                                                                                                                                YSHENLIEDFNSGLIGPLLICKK------GTLTEGGTQKTFDKQIVLLEAVFDESK-
                                                                                                                                                                                                                                 RQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/115,563 FILING DATE: 02-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent Counsel
STREET: 10666 No. US20030008307Alth Torrey Pines Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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The Scripps Research Institute, Office
                                                                                                                           SWSQSSSLMYTVNGYVNGTMPDITVCA---
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ETLVCKELLKPNRIRLGNWEFYPLSKQQL-QYAAT-----DAYASW
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US-09-815-242-11133
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RESULT
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Best Local :
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SEQ ID NO 11133
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                          24 ASYNTSRSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPRSITSSTSYKRFPLSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                      KKWGLASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVL 278
                                                                                                                                                                                                F-----PKTLEKSTALAAIKPIL
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                                                                                                                                                                                                                                                                                                    CRARNFPAMREGGRILYSKTATEVD------KRAMQLIKVLDTKRDE------SGIA 128
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                                                                                                                                                             EDSTLVKVGIGIDGDSVKLFHDYGVSIKDVE------
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                                                                                                                           ENPNIHKIGONIKFDE-SIFARHGIELOGVEFDTMLLSYTLNSTGRHNMDDLAKRYLG--
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant
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                                                     -HETIAFESLAGKGKSQL-TFNQIPL-EQATEYAAEDADVTMKLQQAL
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Pred. No. 3
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318

413

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; ORGANISM: Zea mays US-10-174-363-22
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APPLICANT: CURTIS, ROLY A.J.
APPLICANT: CURTIS, ROLY A.J.
TITLE OF INVENTION: 18610, A NOVEL HUMAN TRANSIENT RECEPTOR
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: MNI-182
CURRENT APPLICATION NUMBER: US/09/920,346
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: USSN 60/221,925
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PASTSEQ for Windows Version 4.0
 Query Match
Best Local Similarity
Matches 66; Conser
                                                                                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/10174363 Publication No. US20030077623A1 GENERAL INFORMATION:
                                                                                                                                                            APPLICANT: Butler, Karlene H.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Harvell, Leslie T.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Gene Silencing
TITLE OF INVENTION: Gene Silencing
TITLE OF INVENTION UMMBER: US/10/174,363
CURRENT APPLICATION NUMBER: US/10/174,363
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/298,973
PRIOR APPLICATION NUMBER: 60/298,973
PRIOR APPLICATION NUMBER: 60/298,973
PRIOR TILING DATE: 2001-06-18
NUMBER OF TELLING DATE: 2001-06-18
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Best Local Similarity
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                                                                                                                                                   NUMBER OF SEQ ID NOS: 56
                                                                                             TYPE: PRT
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 5.8%; ilarity 20.6%; Conservative 4
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ilarity 21.1%;
Conservative 4
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 40;
Score 87; DB 9;
Pred. No. 6.7;
0; Mismatches 9
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95;
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                             Length 910;
Indels 120;
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Gaps
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US-09-741-669-380
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                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 346
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                321
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                                             268
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APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
TITLE OF INVENTION: Genes identified as required
TITLE OF INVENTION: proliferation of E. coli
TILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                          223 -YAKQNNLAYTKL----
                                                                                                                                                                                                                                                                                               127 IAFV-----GLDIEWRPSFRKGV-----
                                                                                                                                                                                                                                                                                                                                                                 107 AVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVV-RRADGSG
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5. US20020022718A1
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                                                                                                                                                                                                                                                                                                                                                                                                                    86 ARNFPAMREGGRILYSKTATEV-----DKRAM----
AYASWHLYKVLKDLPDAV 285
                                                                                                       DLANQKIGGDKKWGLASLTETLVCKELLKPNR----IRLGNWEFYPLSKQ--QLQYAATD
                                                                                                                                                                                                                                                            TSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPGAIGYVEYA---
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                                                                                                                                                                                                        NYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLS----
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                                                   DLTNQK--GEDAWPITSTTFILIHKDQKKPEQGTEVLKFFDWAYKTGAKQANDLDYAS--
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1999-12-23
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; Pred. No. 1.9;
34; Mismatches
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                                                                                                                                                                                                                                                                                                             -----LPGKVATVQICVDS
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; TYPE: PRT
; ORGANISM: Arabidopsis thallana
US-10-268-441-15
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US-10-268-441-15
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TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND PROTEINS AFFECTING STORAGE
TITLE OF INVENTION: ORGANELLE
TITLE OF INVENTION: FORWATION AND METHODS OF USE
TILE REFERENCE: BB1392 US NA
CURRENT APPLICATION NUMBER: US/10/268,441
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/672,607
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157209
PRIOR APPLICATION NUMBER: 60/157209
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Appropriate Publication No.
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Best Local Similarity 31.1
Matches 19; Conservative
                                                    CURRENT APPLICATION NUMBER: US/10/268,441
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/672,607
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157209
PRIOR FILING DATE: 1999-09-30
                                                                                                                                                            APPLICANT: Ripp, Kevin
APPLICANT: Zheng, Petzhong
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND PROTEINS AFFECTING
TITLE OF INVENTION: ORGANILLE
TITLE OF INVENTION: FORMATION AND METHODS OF USE
FILE REFERENCE: BB1392 US N
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                    SOFTWARE: Microsoft Office 97
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                                    NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                          Jung, Rudolf
Li, Chun Ping
Nichols, Scott
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Helentjaris, Timothy George
Jung, Rudolf
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Nichols, Scott
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31.1%;
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Pred. No. 2;
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                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 55
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LENGTH: 593
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APPLICANT:
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308
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Local Similarity 32.1%;
    176
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                                                                                                                    200 --- RRNLIFKVNPTYQRQKFILDYIKTHDEDA-----GIIYCSTRKQVE----ELQEALE 247
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                                                                                                                                                                                                 150 SYQNIISKVFTLPQDFTIIALTATATVEVQQDIREKLNIAQTDQIKTSTK------ 199
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55; Conserv
    QHLIEDSTLVKVG-IGIDGDSVKLF---
                                          SQKIESVIYHAGLSNKEREEAQNDFLFDRVKVVVATNAFGMGIDKSNVRFVIHYNMPGDL 307
                                                                             TKRDESGIAFVGLDIEWRPSFRKGVLPGK----VATVQICVDSNYCDVMHIFHSGIPQSL 175
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Yamamoto, Robert T.
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larity 21.0%;
Conservative 4
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Pred. No. 2.1;
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    HDYGVSIKDVEDLSDLANQKIGGDKKWG 227
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RESULT 11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-74
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; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; CURRENT FILING DATE: 2001-06-26
                                                                                                               GENERAL INFORMATION:
APPLICANT: Broadus, Julie
                                                                                                                                                           Sequence 213, Application US/10108605 Patent No. US20020160934A1
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SEQ ID NO 74
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    APPLICANT: Bachmann, Jane APPLICANT: Kamdar, Kim TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: PROTEI
                                                                                           APPLICANT:
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PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
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                                                                                         Stam, Lynn
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NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
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                      PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR ETILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6900
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LENGTH: 1394
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                                                                                                                                                                             TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
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NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2002-03-27
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ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 QQKIQYRPCTKNQQCSILRINRNRCQYCRLKKCIAVGMSRDAVRFGRVPKREKARILAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 DDELCEQHHQRLDSSQLNYLCQKFDEKLDTALSNSSANTGRNTPAVTANEDADGFFRRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             667 GLFCAIVLITPDRPGLRNLELIEKMYSRLKGCLQYIVAQNRPDQPEFLAKLLETMPD 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LVCK-ELLKPNRIRLGNWE----FYPLSKQQLQY--AATDAYASWHLYKVLKDLPD 283
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OZAKI, AKIO
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TATEISHI, NAOKO
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OCHIAI, KEIKO
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22.4%; Pred. No. 17;
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN PORT 3.0
SEQ ID NO 6005
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6900
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                                                                                         Query Match
Best Local
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                                127 IAFYGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLI-----E 180
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15 VSFVG----
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                                                                                     Similarity
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Similarity 17.0%;
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OZAKI, AKIO
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OCHIAI, KEIKO
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                                                                                    Score 82.5;
Pred. No. 4;
                                                                   Mismatches
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 PETTRHPIRGLVHRD
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                                                                 Gaps
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US-09-391-340-12
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TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES FILE REFERENCE: 09010/027001

CURRENT APPLICATION NUMBER: US/09/391,340A

CURRENT FILING DATE: 1999-09-07

EARLIER APPLICATION NUMBER: US 08/907,166

EARLIER FILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 12

LENGTH: 574
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 50
LENGTH: 389
TYPE: PRT
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Best Local Similarity 21.1%;
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                                                                                                                                                                                                                    APPLICANT: Callen, Walter APPLICANT: Mather, Eric
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Harvell, Leslie T.
APPLICANT: Rafalski, Antoni J.
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Pred. No. 8;
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Copyright (c) 1993 - 2003 Compus
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US-09-896-186B-24
US-09-513-996A-6723
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Sequence 67237, A
Sequence 24, Appl
Sequence 67236, A
Sequence 27138, A
Sequence 2, Appli
Sequence 50, Appl
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ALIGNMENTS

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; OTHER INFORMATION: US-09-513-996A-67237
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APPLICANT: N. ALEXANDROV et al.
 Query Match
Best Local S
Matches 288
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 67237
LENGTH: 288
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID. TITLE OF INVENTION: ENCODED THEREBY FILE REFERENCE: 2750-709P
                                                                                                                                            NAME/KEY: UNSURE LOCATION: 1..288
                                                                                                         FEATURE:
                                                                                                                           OTHER INFORMATION:
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   288;
                  Similarity
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                100.0%; Score 1491; DB 19; 100.0%; Pred. No. 6.7e-154;
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APPLICANT: Joshua Z. Levin
APPLICANT: Ken Philips
APPLICANT: Greg Budziszewski
APPLICANT: Fred Meins
APPLICANT: Fred Meins
APPLICANT: Zhenya Glazov
TITLE OF INVENTION: Methods of Controlling Ge
FILE REFERENCE: PM5-31481A
CURRENT APPLICATION NUMBER: US/09/896,186B
CURRENT APPLICATION NUMBER: US/09/896,186B
CURRENT FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
                                                 US-09-513-996A-67236

; Sequence 67236, Application US/09513996A

; GENERAL INFORMATION:
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: ENCOUNCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCOUED THEREBY
FILE REFERENCE: 2750-709P
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ORGANISM: Arabidopsis
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Pred. No. 6.7e-154;
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US-09-708-427-27138
Sequence 27138, Application US/0
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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                                                                                                                                                                                                                                                          TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CUBRENT APPLICATION NUMBER: US/09/708,427 CUBRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 27138 LENGTH: 313
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 67236
LENGTH: 298
                                                                   Matches
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Best Local Similarity
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE LOCATION: 1..298 OTHER INFORMATION:
                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..313
                                                                                                                                                                               OTHER INFORMATION: Xaa
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281; Conserv
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           DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL 240
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                                                                Score 1439.5; DB 21
Pred. No. 3.4e-148;
1; Mismatches 4;
                                                                                                                                      ID 1820253
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Pred. No. 7.1e-154;
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TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-896-186B-2
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US-09-896-186B-2
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                                                                         Sequence 50, Application US/09906226 GENERAL INFORMATION:
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TITLE OF INVENTION: Methods of Controlling Gene Expression
FILE REFERENCE: PB/S-31481A
CURRENT APPLICATION NUMBER: US/09/896,186B
CURRENT FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Best Local Similarity
Matches 281; Conserv
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APPLICANT: Butler, Karla
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant RNaseD-Like
FILE REFERENCE: BB1467 US NA
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APPLICANT: Ken Phillips
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APPLICANT: Fred Meins
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Pred. No. 3.4e
1; Mismatches
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PRIOR FILING DATE: July 17, 2000
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Microsoft Office 97
SEQ ID NO 50
LENGTH: 313
TYPE: PRI
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 28856
LENGTH: 288
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APPLICANT: N. ALEXANDROV et al.
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Matches
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Best Local Similarity
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CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                              NAME/KEY: UNSURE LOCATION: 1..288 OTHER INFORMATION:
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis
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                                                                                                                                       96.1%; Score 1433; 96.5%; Pred. No. 1
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RESULT 9
US-09-513-996A-28857
Sequence 28857, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FILE REFERENCE: 2750-709P
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT APPLICATION NUMBER: SEQ ID NO 28857
LENGTH: 197
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US-09-513-996A-67238
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Best Local S
Matches 197
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APPLICANT: N. ALEXANDROV et al.
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SEQ ID NO 67238
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FEATURE:
NAME/KEY: UNSURE
LOCATION: 1..197
OTHER INFORMATION: any
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TYPE: PRT
ORGANISM: Arabidopsis thaliana FEATURE: NAME/KEY: UNSURE
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100.0%; Pr
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; Pred. No. 2.1e-103;
0; Mismatches 0;
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US-09-708-427-27139
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27139
LENGTH: 222
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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Best Local Similarity
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Best Local Similarity
Matches 191; Conserv
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NAME/KEY: misc_feature
LOCATION: 1..222
OTHER INFORMATION: Xaa
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LOCATION: 1..222
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OTHER INFORMATION: any n
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Pred. No. 1.2e
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Pred. No. 6.9e-100;
2; Mismatches 4;
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RESULT 12
US-09-708-427-27140
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APPLICANT: N. ALEXANDROV et al.
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 28858
                                                                                                         Query Match
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                          EQ ID NO 27140
LENGTH: 202
TYPE: PRT
                                                                                                                                                FEATURE:

NAME/REY: misc_feature

LOCATION: 1..202

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..202

OTHER INFORMATION: Ceres Seq. ID 1820255
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                                                                                                                                                                                                                                                        ORGANISM: Arabidopsis thaliana
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Pred. No. 5.4e-89;
                                                                           Score 876.5; DB 21; Pred. No. 9.1e-87; 1; Mismatches 4;
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SOFTWARE: Microsoft Office 97 Page 1D NO 16
                            NUMBER OF SEQ ID NOS:
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US-09-906-226-16
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US-09-620-393B-6113
                                                  APPLICANT: Butler, Karla
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant RNaseD-Like Genes
FILE REFERENCE: BB1467 US NA
CURRENT APPLICATION NUMBER: US/09/906,226
CURRENT FILING DATE: 2001-07-16
CURRENT FILING DATE: 2001-07-16
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APPLICANT: ALEXANDROV, Nickolai et al.
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                                                                                                                                                                                                                                          Sequence 16, Application US/09906226
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
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PRIOR APPLICATION NUMBER: 60/218993
PRIOR FILING DATE: July 17, 2000
NUMBER OF SEO ID NOS: 57
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NAME/KEY: misc_feature
LOCATION: 1...157
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Sequence 16, Application US/60218993
GENERAL INFORMATION:
APPLICANT: Butler, Karla
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant RNASeD-Like Genes
FILE REFERENCE: BB1467 US PRV
CURRENT APPLICATION NUMBER: US/60/218,993
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 22
SOFTMARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 290
TYPE: PRT
ORGANISM: Glycine max
US-60-218-993-16
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; ORGANISM: Glycine max
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Matches 139
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113 TDMMQTAIGFDIEWKPTFRKGVPPGKVAVMQICGDTRHCHVLHLIHSGIPQNLQLLLEDP 172
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Similarity 49.3%; Pred. No. 1.4e-64;
39; Conservative 49; Mismatches 63;
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                                                            TVLKVGAGIDGDAVKVFRDYNISVKGVTDLSFHANQKLGGDHKWGLASLTEKLLSKQLKK 232
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Search completed: June 6, 2003, 10:30:14 Job time: 309 secs

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Maximum Match 100%
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RESULT 2 US-09-724-676-89006

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RESULT 3
US-09-724-676A-89006
Sequence 89006, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE RÉFERENCE: 129181.4 Compugen US/09/724,676A
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN version 3.2
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; ORGANISM: Homo sapiens
US-09-724-676-89006
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US-09-724-676A-89006
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LENGTH: 994
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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75; Conserv
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                                   DAYASWHLYKVLKDLPDAV 285
DAYAGFIIYRNLEILDDTV 234
                                                                            KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT
                                                                                                                KDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
                                                                                                                                                            KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 352; DB 5; Pred. No. 3.5e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09949001 GENERAL INFORMATION:
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 22
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT APPLICATION NUMBER: U$/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION
FILE REFERENCE: CLO00789
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 848 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                        LENGTH: 14
TYPE: PRT
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KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
                                                                                             DAYAGFIIYRNLEILDDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNFVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT
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                                                                    DLPFLEFTGSIVYSYDASDCSFLSE-----DISMSLSDGDVVGFDMEWPPLYNRGKL-G
                                                                                                                                             Conservative
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                                                                                                                                                              23.6%;
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37.7%; Pred. No. 5.5e-22;
ive 41; Mismatches 75;
                                                                                                                                           Score 352; DB 5; 1
Pred. No. 5.7e-22;
1; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
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US-10-374-077-71
Sequence 71, Application US/10374077
GENERAL INFORMATION:
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Matches
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INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 1432 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:

CORRESPONDENCE SEED Intellectual Property Law Group
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: ANTIBODIES AGAINST GENE PRODUCTS RELATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/374,077
FILING DATE: 25-Feb-2003
CLASSIFICATION: CUMKNOWN>
ATTORNEY/AGENT INFORMATION:
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       216
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                                                                                                                                                                                                                                                                                                                        Similarity
                         DAYASWHLYKVLKDLPDAV 285
                                                                                                                                                                   KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
     DAYAGFIIYRNLEILDDTV 234
                                                                         KNEVELTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNWSKFPLTEDQKLYAAT
                                                                                                                                                                                                                         DLPFLEFTGSIVYSYDASDCSFLSE-----DISMSLSDGDVVGFDMEWPPLYNRGKL-G
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                                                                                                            KDVEDLSDLANQKIGGDKKWGLASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAAT 266
                                                                                                                                                   KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rosenman, Stephen
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 100107.401D1
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                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                               23.6%; Score 352; DB 6; L
37.7%; Pred. No. 5.7e-22;
Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                      Length 1432;
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                             US-10-424-599-238476; Sequence 238476, Application US/10424599; GENERAL INFORMATION:
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US-10-374-077-206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 1401 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/374,077
FILING DATE: 25-Feb-2003
CLASSIFICATION: - CURKOWN>
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schellenberg, Gerald D.
TITLE OF INVENTION: ANTIBODIES AGAINST GENE PRODUCTS RELATED
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 100107.401D1 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                    264 AATDAYASWHLYKVLKDLPD 283
                                                                                                                                                                                                                                                          204 VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                                                                             87 KRSRVAVIOLCVSESKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD 146
                                                                                                                                                                                                                                                                                                                                                                         37 NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                                                                                            88 NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 72; Conserv
La Rosa Thomas J
Kovalic David K
                                                                                                                                               AATDAYAGLIIYQKLGNLGD 226
                                                                                                                                                                                                                         VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 43,058
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Oshima, Junko
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Length 1401; Indels

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Gaps

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206 263

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us-09-8

...FLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 238476

LENGTH: 238

TYPE: no--
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US-10-424-599-238476
                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 700346357_FLI.pep US-10-425-114-37706
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37706
LENGTH: 210
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Best Local
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                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                          Local Similarity
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Local Similarity 39.9%;
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                                                                                                  140 FRKGVLPGKVATVQICVDSNYCDVMHIFHSG-IPQSLQHLIEDSTLVKVGIGIDGDSVKL 198
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ENDYDLEVANAEDLAELAAKEMGRPDLRNAGLQGIARAVMDAHVEKPQWVRTGPWDASSL
                               FHDYGVSIKDVEDLSDLANQKIGGD--KKWGLASLTETLVCKELLKPNRIRLGNWEFYPL 256
                                                                                                                                    PMAATKVCN---VRFEGNVITTTVTASGAAVESWLDEILSVHRRRLHKLVVGLDVEWRPS
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Screen, Steven E
Tabaska, Jack E
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                                                                  FSRAY -- SKTAIVOLCV-GRRCLIFQLLHADYVPNTLDEFLSDPDYTFVGVGVAADVERL
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28.7%;
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Pred. No. 2.8e-14;
98; Mismatches 56;
                                                                                                                                                                                                                      Score 249.5; DB 6;
Pred. No. 5.5e-14;
                                                                                                                                                                                                        Mismatches
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RESULT 11
US-10-424-599-191095; Sequence 191095, A
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US-10-425-114-71107
; Sequence 71107, Application
                                           ; FEATURE:
; OTHER INFORMATION: Clone
US-10-424-599-191095
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 71107
LENGTH: 236
TYPE: PRT
                                                                                                                                                      NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191095
LENGTH: 208
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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Best Local Similarity
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof fc
FILE REFERENCE: 38-21(53313)B
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                                                                                                       ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 VQICVDSNYCDVMHIFHSG-IPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVE 210
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Screen, Steven
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28.9%;
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                                                                   ID: PAT_MRT3847_14578C.1.pep
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Pred. No. 1.
Score
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LENGTH: 205
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                                                                                                                                               FILE REFERENCE: PATH03-08
CURRENT APPLICATION NUMBER: US/10/431,652
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 09/328,352
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 60/088,701
PRIOR APPLICATION NUMBER: US 60/088,701
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)8
FULL REFERENCE: 38-21203-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
RUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                     APPLICANT: Breton, Gary L.

APPLICANT: Bush, David

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                  PRIOR FILING DATE:
                                       ORGANISM: Acinetobacter baumannii
                                                            TYPE: PRT
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                                                                             LENGTH: 223
                                                                                              ID NO 6289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 188; DB 6;
Pred. No. 1.5e-08;
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1; Mismatches 60;
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Best Local
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
                                                                                      CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
                                                                                                                       APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-030
                                                    PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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RESULT 14
US-10-425-114-71315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 71315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 198
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 VGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 FVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIP--QSLQHLIEDSTLVK 186
                                                                                                                                      173 QSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG--VSIKDVEDLSDLANQKIGGDKKWGLAS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 FLGFDSESKPTFQVGEVSTGPHLIQLATEHK----AYLFHVNLSTLKFLQPILSNPKQIK 113
                                                                                                                                                                                                                                                                                  l Similarity
47; Conserv
                                                                                                                                                                                     1 LNATSDIEACKIIGMDCEWRPNFEKNTKSSKVSIIQIASDKIAFIFDLIKLYEDDPKALD
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LSKEILGAGLNKTR--RNSNWEQRPLTQNQKEYAALDAVVLVHIF 161
                                         LTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLY 275
                                                                                          SCLRRVMCSSKILKLGYDIQCDLHQLTRSYGELECFQSYEMVLDM--QKLFKGVTGGLSG 118
                                                                                                                                                                                                                                 LDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVD--SNYCDVMHIFH---SGIP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSNWARKPLTSQQISYAAADAYAALLVFLELKKRKVLPIHIS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKD---LPDAVS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGFGLKNDK-HIFHKKGIELESCVDLAK-GFSHFGFKQQMGVQKAVALLLGQYLAKSKKV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screen, Steven E
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27.6%;
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                                                                                                                                                                                                                                                                                  Score 163.5; DB 6;
Pred. No. 2.1e-06;
Pred. No. 74;
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Polypeptides